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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 02:26:33 ; Search time 85 Seconds
(without alignments)
7978.235 Million cell updates/sec

Title: US-10-019-661-1
Perfect score: 1222
Sequence: 1 cttactgtattgtttatt.....tcatttgggtcttttgcgt 1222

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	52	4.3	7218	1	US-08-232-463-14
2	49.4	4.0	10467	4	US-10-204-708-2
3	48.8	4.0	19124	2	US-08-487-828B-13
4	45.8	3.7	936	4	US-09-328-352-1255
5	45.6	3.7	15016	4	US-09-601-198-60
6	45.2	3.7	53332	4	US-09-801-861-3
7	45	3.7	5152	4	US-10-204-708-73
8	44.8	3.7	5562	4	US-10-204-708-63
9	44.2	3.6	8961	4	US-10-204-708-80
10	44	3.6	5181	1	US-08-257-073-10
11	43.8	3.6	658	3	US-08-998-416-595
12	43.4	3.6	6156	4	US-10-204-708-60
13	43	3.6	10640	4	US-09-417-485D-5
14	42.6	3.5	6243	2	US-09-056-075-1
15	42.4	3.5	1563	4	US-09-508-370A-11
16	42.2	3.5	471	1	US-08-248-466B-5
17	42	3.5	1720	1	US-08-248-466B-2
18	42	3.4	1320	3	US-08-257-073-15
19	42	3.4	1482	3	US-08-098-327E-41
20	42	3.4	1482	3	US-08-098-327E-45
21	42	3.4	1482	4	US-08-462-625-41
22	42	3.4	1482	4	US-08-462-625-45
23	42	3.4	1493	3	US-08-098-327E-38
24	42	3.4	1493	4	US-08-462-625-38
25	42	3.4	4702	4	US-08-956-171B-268
26	41.8	3.4	6317	4	US-10-204-708-12
27	41.8	3.4	19513	4	US-10-204-708-40

C 28	41.6	3.4	4544	4	US-08-956-171E-517
29	41.6	3.4	5501	4	US-10-204-708-38
C 30	41.4	3.4	2447	2	US-09-014-969-14
31	41.4	3.4	4818	3	US-08-817-926-27
32	41.4	3.4	5340	4	US-09-627-122-21
33	40.8	3.3	6583	4	US-10-204-708-26
C 34	40.8	3.3	1664976	4	US-08-916-421B-1
C 35	40.6	3.3	7218	1	US-08-232-463-14
36	40.6	3.3	19233	4	US-10-204-708-45
37	40.2	3.3	726	3	US-08-998-416-183
C 38	40.2	3.3	1939	1	US-07-715-751B-2
39	40.2	3.3	6669	4	US-10-204-708-6
40	40.2	3.3	7295	2	US-08-487-826B-15
C 41	39.8	3.3	240	1	US-08-628-417-6
C 42	39.8	3.3	1051	3	US-09-245-041-10
C 43	39.8	3.3	1696	4	US-09-835-811-1
C 44	39.8	3.3	6243	2	US-09-056-075-1
C 45	39.8	3.3	640681	4	US-09-790-988-1

ALIGNMENTS

RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14
Query Match 4.3%; Score 52; DB 1; Length 7218;


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; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-487-826B-13

Query Match          4.0%; Score 48.8; DB 2; Length 19124;
Best Local Similarity 48.0%; Pred. No. 0.019;
Matches 169; Conservative 0; Mismatches 182; Indels 1; Gaps 1;

Qy 841 TTTAAATGATTTTAAATAGTTATAAATCTTTTGTAGAACTATCTTCATTTAATTGAT 900
Db 15985 TGTATATGTCATGTAATTAATTTATTTTATTTTATTTTAAATTAATTAATTTTATTT 15926

Qy 901 AGTACGTAAGGTTTACATCATCTAGGAGTATCTGTGAGCAATCATCACTTCGTTACTGT 960
Db 15925 TTTTATTTTATTCATTAATTTTAAATTTTATTTTATTTTATTTTAAATTTTATTTAT 15866

Qy 961 GATGGTCAACTACCATATGAAATATTTTATTAAGTCCCATCTCGAAAGTAATCCACA 1020
Db 15865 TATTTTATTTTATTTA-ATTAATTTTATTTTATTTATTTATTTTATTTTAAATTAAT 15807

Qy 1021 TATCACAGTCTATTAATCTGATCTCTTCATCTAATGTTAATTTTCCCTTTTGGGG 1080
Db 15806 TTTTATTTATTTATGATATATATTTTATTTTAAACATTTTATTTTAAATTTTATTTATG 15747

Qy 1081 TATCCATACGTTAATGAATCTTTTAAATTCATCTGTTTGTGAGAAAGATATCTTTT 1140
Db 15746 ATATATATTTTATTTAATTAATTTTCTTTTCTTTTGTGTTTATGATATATATTT 15687

Qy 1141 TTGTTTAAATGACGACATGATATCTTTTATTTCTTGTGTTTCCCTAAAAA 1192
Db 15686 TTTTATTTTAAATGTTTATTTTCTTTCTTTGTTGTTTATTTTATTTTATTA 15635

RESULT 4
US-09-328-352-1255
; Sequence 1255, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1255
; LENGTH: 936
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1255

Query Match          3.7%; Score 45.8; DB 4; Length 936;
Best Local Similarity 47.4%; Pred. No. 0.037;
Matches 137; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

Qy 157 TGTATCTTTTGGACATCGAAGAGGACCTTTTATAGATACAGGTATGCCAAGAT 216
Db 223 TGTCTTTTGGTAGAACTATCGAGGCGCTTGTACTGATGATACCGGATTTGGCCTACAA 282

Qy 217 GCAGTTAATAATGAAGGCTTTTAAACGGTACATTTGTCGAAGGCGCAGGTTTACCGAAA 276
Db 283 GATTATCTACATCGAACACGGCTTGGCTCTTTAGTCAAAACGGTTGGGGAAAAATTGAA 342
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Qy 277 ATGACTGAAGAAGATAGAAATCGTGAATATTTTAAACGGGTTGTTATAGCCCGAAGAC 336
Db 343 CCGAATCTTGAGTTCACTGCTGCTATTCAACAAATTCAGAAATCGGGTTTCCATCCTAAGAT 402

Qy 337 CTTCCTTTATATTAGTTCTCACTTGCATTTTGCATCATGAGGAGGAATGGCGCTTTT 396
Db 403 GTGCAGCACATTTTGTGACTCACTCGACTTTGACCATGACCATGAGGCGGAATTTTCAGACTTT 462

Qy 397 ATAAATACCAATCATTTGTACGCTGCTGAATATGAGGCGGCGCAGC 445
Db 463 CCCACGCCACTGTCCATGCTAGTACTGATACATCAATGCTGCGCAAC 511

RESULT 5
US-09-601-198-60
; Sequence 60, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
; APPLICANT: Cassell, Gail H.
; APPLICANT: Chen, Ellison Y.
; APPLICANT: Glass, Jennifer S.
; APPLICANT: Glass, John I.
; APPLICANT: Heiner, Cheryl R.
; APPLICANT: Lefkowitz, Elliot
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
; FILE REFERENCE: UAB-13452/22
; CURRENT APPLICATION NUMBER: US/09/601,198
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/073,189
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 15016
; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-60

Query Match          3.7%; Score 45.6; DB 4; Length 15016;
Best Local Similarity 47.5%; Pred. No. 0.11;
Matches 172; Conservative 0; Mismatches 184; Indels 6; Gaps 1;

Qy 786 CCTGGAATATATATAGTACAAAAGTCATGAGCTTATTCGCTCATGACTTTTTCGTTTAA 845
Db 14646 CCCAGATCAACTTCATTATTATGTTTAACTGAATTATCAACATCATCTGAACTAATA 14705

Qy 846 ATGATTTTTTAAATAAGTTATAAATCTTTTGTAGAACTATCTTCATTTAATTGATAGTAC 905
Db 14706 ATTGTTTCTTTAGGAATGATGATATTCATCTTCTATGCTAATGAATCAAAATGATAATC 14765

Qy 906 GTAAGGTTTACATCATTAGAGTATCTGTTGAGCAATCATCACTTCGTTACTCTGATGG 965
Db 14766 TTATCTTTTGTAAAATTTAGGGTGTGTTGATAGATCAATTTGTACTGCTGTTATTATTA 14825

Qy 966 TCAACTACCATATGAAATATTTTTTATAAGTCCATCCCTCGAAAGTAATCCACATATCA 1025
Db 14826 ACAATTCAGGAATTTTATCAAAATTAACCATCAACTCTGGTAAATTAACAAAAACGTCT 14885

Qy 1026 CAGTCTATTAATCTGATCCTTCTTCATCTAATGTTAAT-----TTTCCTTTTTCGGG 1079
Db 14886 TCGCCTTTCTTCAACATTTTGTGCGACATCAAAATCAATTAATGGTTATTAACAATTTTACCA 14945

Qy 1080 GTATCCATACCTGTTTAATGAATGTTTTTAAATTCATCTGTTTTTGTGAGAAAGATATCCTTT 1139
Db 14946 ATATTAGTTTGTAAACAATTAATTTGTTTTGTATCCAAATCAGCAACATTAATTTACTTTT 15005

Qy 1140 TT 1141
Db 15006 TT 15007
```

RESULT 6

US-09-801-861-3
; Sequence 3, Application US/09801861
; Patent No. 6492154
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801.861
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53332
; TYPE: DNA
; ORGANISM: Human
US-09-801-861-3

Query Match 3.7%; Score 45.2; DB 4; Length 53332;
Best Local Similarity 46.2%; Pred. No. 0.2;
Matches 184; Conservative 0; Mismatches 213; Indels 1; Gaps 1;

Qy 797 TATAGTACAAAAGTCATGAGCTTATTCGCTCATGACTTTTCGTTTAAATGATTTT 856
Db TTTAATAATAATTCCTAAAATGGCAATCAGTATATTTTATATATATATATATAT 31340

Qy 857 AAATAAGCTTATAAAGCTTTTATAGAACATCTCTTCAATTAATGATGACGTTTAC 916
Db ATATTTTAT 31340

Qy 917 ATCAATAGGAGTATCTTGTTGAGCAATCACTCGCTGATGAGTGGTCACTACCA 976
Db ATATTTCTAT 31460

Qy 977 TATGABATATTTTATAAGTCCCATCTCGAAGAGTATCCACATATACAGTCTATTA 1036
Db TATTTTAT 31519

Qy 1037 ATCTGATCTCTTCTCATCTAATGTTAATTTTCTTTTGGCGGTATCCATACGTGTTAAT 1096
Db ATTAT 31579

Qy 1097 GAATGTTTTTAATTCATCTGTTTTGAGAGAAATATCCTTTTGTGTTAATGATC 1156
Db ATATTTTAT 31639

Qy 1157 GACATGATATCTTTTATTTCTGTTTCTTAAAGAA 1194
Db TAT 31677

RESULT 7

US-10-204-708-73
; Sequence 73, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204.708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7

; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 73
; LENGTH: 5152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-73

Query Match 3.7%; Score 45; DB 4; Length 5152;
Best Local Similarity 43.4%; Pred. No. 0.1;
Matches 255; Conservative 0; Mismatches 330; Indels 2; Gaps 1;

Qy 604 GTATTATTAACGATTGATGATCGATCGATACGAAAGAGAAATTTGAAAATGAAGTCCCATTT 663
Db GTGATTTTAAAGTTAATTTTAAATTAATATATATATATATATATATATATATATATATATAT 3547

Qy 664 GCGGGATTTCAGTTCAGNAATTAGCTTTTATCTTCAATTAACGTTTAAAGAGTGTGAT- 722
Db TATTTTATAGTTTAAAGGAGATTTTATATTAATTTTAAATTAAGAGTTGGAAATATATC 3607

Qy 723 -GAAAGAGAGCCGATTTCTTTGGACATGATATAGACAGAGAAAGGGGATGTAAAG 781
Db GTTTAAAGATTTTGAATTTTGTAAAGTAAAGAAATAGTAAATATAGTTTGTAAAG 3667

Qy 782 TGTTCCTGTAATATATATAGTACAAAAGATCATGAGCTTATTCGCTCATGACTTTTTCGT 841
Db ATTAGAAATTTATAGTGTAGTAGTGTGTTTAAATATATATATATATATATATATATATAT 3727

Qy 842 TTAATGATTTTTTTTAAATAGTATTAAGCTTTTTTAAAGTATCTTTCATTTAATTCGATA 901
Db AAAAATGGGAAAATTTTTTATAAATTAAGATGTGTTAAAGGAAATAGTATTTAATGAAA 3787

Qy 902 GTACGTAAAGGTTTACATCATTTAGGAGTATCTTGTGAGCAATCATCACTTGTACTGTG 961
Db ATATTTTATTTTAAATTTTAGGTGTTAAAGAAATGATTTTAAATGTTGCTGTAATAA 3847

Qy 962 ATGTCACATCCCATATAGAAATATTTTTTATAGTCCCATCCCTCGAAAGTAAATCCACAT 1021
Db ATTGTATATATATATTTTGAATTTAAATTAAGTTAAATTTTAAAAATATAAAATATAAA 3907

Qy 1022 ATCACGCTCTTAAATCTCATCTCTTCAATCTAATGTTAAATTTTCTTTTGGCGGT 1081
Db AATAAAAAATTTTAAAGTATTTTTTAAATATAGTATAATTAAGTATATGATGCGGT 3967

Qy 1082 ATCCATACTGTTAATGAATGTTTTTAAATTCATCTGTTTTTGTGAGAAAGATATCCTTTT 1141
Db GTTATTTTATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTG 4027

Qy 1142 TGTTTTAAATGACTCGACATGATATCTTTTATTTCTTTCTTTTCTTA 1188
Db TTTTCTTTAGGTTGAAATGTAGTGGCTAAATACGGTTTATGATA 4074

RESULT 8

US-10-204-708-63
; Sequence 63, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204.708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8


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; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 63
; LENGTH: 5562
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
;   - OTHER INFORMATION: Chemically treated
US-10-204-708-63

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Query Match	3.7%;	Score 44.8;	DB 4;	Length 5562;
Best Local Similarity	47.0%;	Pred. No. 0.12;		
Matches 171;	Conservative 0;	Mismatches 192;	Indels 1;	Gaps 1;
QY	819	TTATTCGCTCATGACCTTTTTCGTTTAAATGATTTTTTAAATAGTTATAAACCTTTTTTA	878	
Db	1401	TTATTAATTTTTTTTTTCGGTTAGGAATGATTTTTTTTTTGATATATTATTAATTTTTT	1460	
QY	879	GAACTACTTCATTTAAATTCATAGTAGCTAAGGTTTACATCATTAGGAGTATCTTGTTGA	938	
Db	1461	TATTTTAGTTAGTTTTTTTTTTTTTTTATTTTATTTTATTTTATTTTGTGTAGT	1520	
QY	939	GCAATCATCACTCGTTACTGTGATGTCGACTACCCATATGAATAATTTTTTATAAGTC	998	
Db	1521	TAGATTTTTTTTTTTTTTATTTTGTGTTTTTATA - GTGTGTTTTTTTTTATTTTTTTT	1579	
QY	999	CCATCCTCGAAAGTAATCCACATATCACAGCTATATAAATCGATCCTCTTCATCTAAT	1058	
Db	1580	TTGTTTAAAGAAAGTTATTAATTTTATTTTATTTTATTTTATTTTATTTTAGGATAGT	1639	
QY	1059	GTTAAATTTTCCCTTTTTTGGCGGTATCCATACGTGTTAAATGAATGTTTTTAATCATCTGTT	1118	
Db	1640	GTTATTTTTAGAAATTTTGATATAATGAATTTTATTAATTAATTTTGTGTTTTTTT	1699	
QY	1119	TTTGTGAGAAGATATCCCTTTTTTGTGTTTTTAATTCGACTCGACATGATATCTTTATTTCT	1178	
Db	1700	TTATTTATGATGGTTTTTTTTTTTTTTTTTTTTTTTATTTGATTTTTTTTACGTTTTTCG	1759	
QY	1179	TGTT 1182		
Db	1760	TTTT 1763		

RESULT 9
US-10-204-708-80
; Sequence 80, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS:98

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; SEQ ID NO 80
; LENGTH: 8961
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (5096)
; OTHER INFORMATION: n is a o r g o c o r t
US-10-204-708-80

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Query Match	3.6%;	Score 44.2;	DB 4;	Length 8961;
Best Local Similarity	43.4%;	Pred. No. 0.2;		
Matches 202;	Conservative 0;	Mismatches 263;	Indels 0;	Gaps 0;
QY	674	ATTGAGAAATGAGCTTTATCTTTCAATTAAACGTTTAAAGAAAGTGGTGATGAAAGAGAAGC	733	
DB	5190	ATTTGTTTTTATATATTT	5249	
QY	734	CGATTGTTTCTTTGGACATGATATGAGCAGGAAGGGGATGTAAAGTGTTCCTCGAAT	793	
DB	5250	TATATATATATGTTAGAGATGTGTGATATTTTAAATATTTGTAGATTTTTTGTAAATTAAT	5309	
QY	794	ATATATAGTACAAAAAGTCATGAGCTATTTCGCTCATGACCTTTTCGTTTTAAATGATTTTT	853	
DB	5310	TTTTTTTAGATATTTTATATATAGATATTTTTTGTAAATTTTTTTTTTATTTTCGATTTAA	5369	
QY	854	TTTTAAATAAGTTATAAACCTTTTTTAGAATCATCTTCATTTAATGTATGACGTAAAGTT	913	
DB	5370	TGTTAATATTTTATAATAATTTAATATTTTTTTTTTTTATGCTTATTTTATATAAAGTA	5429	
QY	914	TACATCATTAGGAGTATCTGTTGAGCAATCATCACTTCGTTACTGTGATGGTCAACTAC	973	
DB	5430	TTTTTCGTAGTATTATGTTTTATATTTTATAATTTTAGTTTTTATTTTTTATAGATATT	5489	
QY	974	CCATATGAATAATTTTTTATAAGTCCCATCTCGAAAGTAATCCACATATCACAGTCTAT	1033	
DB	5490	TTATAATAATTAATTTTTTATTTTATTTTAGTTTGATATTTTATAATAGTTAGAAAATTTAT	5549	
QY	1034	TAAATCTGATCCTCTCTTCATCAATCTTAATTTTTTCCTTTTTTGGCGGTATCCCATCTGTT	1093	
DB	5550	TTTTTTTTTATATATAAATACGGATATTCGGTTTTTTTTTATATATATATTTTCGTAATAATT	5609	
QY	1094	AATGAATGTTTTTAAATCATCTGTTTTTGTGAAAAGATATCCTT	1138	
DB	5610	AGTTTTTTTATTTTTTATATTTGATATTTTTTATAAATAATTAATTTTTT	5655	

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1  RESULT 10
2  US-08-257-073-10/c
3  ; Sequence 10, Application US/08257073
4  ; Patent No. 5766597
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Paoletti, Enzo
7  ; APPLICANT: de Taisne, Charles
8  ; APPLICANT: Tine, John A.
9  ; TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
10 ; NUMBER OF SEQUENCES: 143
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESSEE: Curtis, Morris & Safford, P.C.
13 ; STREET: 530 Fifth Avenue, 25th Floor
14 ; CITY: New York
15 ; STATE: New York
16 ; COUNTRY: UNITED STATES OF AMERICA
17 ; ZIP: 10036
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: US/08/257,073

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FILING DATE: 09-JUN-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/075,783
 FILING DATE: 11-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/852,305
 FILING DATE: 18-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/672,183
 FILING DATE: 20-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2570
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 TELEX: 425066 CURTMS
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5181 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-257-073-10

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US-10-204-708-60
; Sequence 60, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 60
; LENGTH: 6156
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-60

Query Match      3.6%; Score 43.8; DB 4; Length 6156;
Best Local Similarity 48.1%; Pred. No. 0.22;
Matches 189; Conservative 0; Mismatches 197; Indels 7; Gaps 2;

Qy 741 TTTCTTTGGACATGATAGAGCAGGAAAGGGAGTGAAGAGTTCCTCGAATATATATA 800
Db 5571 TTTAGTTTTTTTAAATTTTAAAGTAAAGATTTAGTTAAAGATTTAGTTATTTT 5630
Qy 801 GTACAAAAGTCATGAGCTTATCGCTCATGACTTTTCGTTTAAAT-GATTTTTTAAA 859
Db 5631 GTATGTATATTTTAAAGTTTTTATTATTTTAAAGTTGTAGATTAAATAGATATATA 5690
Qy 860 TAAGTTATAAATTTTTTTAGAACTATCTTCAATTTTAAATGATAGTAGTAAGTTACATC 919
Db 5691 TTGTAATTTAGTATATTTTAAATTTTAAAGTTTGTAGTTTTTTGTTTATTTT 5750
Qy 920 ATTAGGAGTATCTTTGTTGAGCAATCATCACTTCGTACTGTGATGGTCAACTACCCATAT 979
Db 5751 TTTTATAGTTAAATTTTAAATTAAGATGATGATGATGATTTTGTATATTTAAATTT 5810
Qy 980 GAAATATTTTTTAAAGTCCCATCTCGAAAGTAATCCACATATCACAGTCTATTAATC 1039
Db 5811 TAAGAAATTTATAGTCGTAATTAATTAATAGATTAGTTTAAATTTTGGTTTTAGGATAG 5870
Qy 1040 TGATCCTTCTCATCTA-----ATGTTAAATTTTCCTTTTTGGGGTATCCATCTTT 1093
Db 5871 TATTGTTATGTTTATTAATAAATAGTTATTTATTTTATTTTGTGTAATATGATTTTATT 5930
Qy 1094 AATGAATGTTTAAATTCATCTGTTTTTGTGAG 1126
Db 5931 TATTGTTATTTGTAATATATATGAGTTGTAAG 5963

RESULT 13
US-09-417-485D-5/c
; Sequence 5, Application US/09417485D
; Patent No. 6541202
; GENERAL INFORMATION:
; APPLICANT: Long, David M.
; APPLICANT: Metz, Anneke M.
; APPLICANT: Love, Ruschelle A.
; TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
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; FILE REFERENCE: 47714-5009-US
; CURRENT APPLICATION NUMBER: US/09/417,485D
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10640
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (834)..(7385)
; OTHER INFORMATION: TERT gene
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1821)..(1837)
; OTHER INFORMATION: m at position 1821 = a or c; w at position 1837 =
; OTHER INFORMATION: a or t. Xaa (amino acid) at position 330 = Leu or
; OTHER INFORMATION: Ile; Xaa at position 335 = Asp or Gly.
US-09-417-485D-5

Query Match      3.6%; Score 43.4; DB 4; Length 10640;
Best Local Similarity 47.5%; Pred. No. 0.33;
Matches 162; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

Qy 852 TTTTAAATAAGTTATATAAATCTTTTAAAGAACTATCTTCATTTAATTTAGTAGTAGTAAAG 911
Db 2433 TTGCTATATTTATAATATAGATATTTTATTTATTTGTAATCTTATAATTTTAAATATTT 2374
Qy 912 TTTACATCATTTAGGAGTATCTTTGTTAGCAATCATCACTTCGTTACTGTGATGTCACACT 971
Db 2373 TATGTAATCTTTTAAATATAATGTTTTCGAGGAAAAAATTTTCTATATATTTTACCAATTT 2314
Qy 972 ACCATATGAAATATTTTATATAAGTCCCATCTCGAAAGTAATCCACATATC---ACAG 1028
Db 2313 TTGTAATTAATTACATTTAATAAATTCCTTAAAAATTAATATATATATTTCAAGATTT 2254
Qy 1029 TCTATTAATCTGATCCCTCTTCATCTAAATGTTAAATTTTCCTTTTTGGCGGTATCCATA 1088
Db 2253 TCGCTTTTCTAGCTGTTTATTTATATTTTGGATGTTTATAATTTTCAAGTTTTTGTGA 2194
Qy 1089 CTGTTAATGAATGTTTTTAAATTCATCTGTTTTTGTGAGAAAGATATCCTTTTTTGTGTTTA 1148
Db 2193 CATGAAATAAATGATTTCTTCTCGATGTAATATATAGAGATATGTCATTTTTTTTGG 2134
Qy 1149 ATTGACTCGACATGATATATCTTTTATTTCTGTTTCTCTAA 1189
Db 2133 TTGAACATTTTATTTGTTTACATATTTTCTGCTTATATTCOA 2093

RESULT 14
US-09-056-075-1/c
; Sequence 1, Application US/09056075
; Patent No. 5953368
; GENERAL INFORMATION:
; APPLICANT: Johnson, Eric A.
; APPLICANT: Bradshaw, Marite
; APPLICANT: Rood, Julian
; TITLE OF INVENTION: Expression System for Clostridium
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```


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OM protein - protein search, using sw model

Run on: February 20, 2004, 16:22:42 : Search time 35 Seconds
(without alignments)
1843.233 Million cell updates/sec

Title: US-10-019-661-2

Perfect score: 1315

Sequence: 1 MTVKLYFVPAGRCMLDHS.....VFFGHDIQERGCKVFPEYI 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1315	100.0	250	2	Q9L8R8	Q9L8R8 bacillus sp
2	1280	97.3	250	2	Q8KWS6	Q8KWS6 bacillus sp
3	1270	96.6	250	2	Q8KTW5	Q8KTW5 bacillus th
4	1256	95.5	250	2	Q8KNY1	Q8KNY1 uncultured
5	1244	94.6	250	2	Q8RPW5	Q8RPW5 bacillus th
6	1230	93.5	250	2	Q8KTW9	Q8KTW9 bacillus th
7	1230	93.5	250	2	Q8KI79	Q8KI79 bacillus th
8	1228	93.4	250	2	Q8RPW6	Q8RPW6 bacillus th
9	1227	93.3	250	2	Q8KTW6	Q8KTW6 bacillus th
10	1222	92.9	250	2	Q8KTW8	Q8KTW8 bacillus th
11	1220	92.8	250	2	Q8KTW3	Q8KTW3 bacillus ce
12	1219	92.7	250	2	Q8RPW9	Q8RPW9 bacillus sp
13	1216	92.5	250	2	Q8KTX1	Q8KTX1 bacillus th
14	1213	92.2	250	2	Q8RPW7	Q8RPW7 bacillus th
15	1212	92.2	250	2	Q8RJA0	Q8RJA0 bacillus th
16	1209	91.9	250	2	Q8RPW4	Q8RPW4 bacillus th

17	1208	91.9	250	2	Q8KTW4	Q8KTW4 bacillus th
18	1206	91.7	250	2	Q8KTX0	Q8KTX0 bacillus th
19	1202	91.4	250	2	Q8RPW8	Q8RPW8 bacillus th
20	1200	91.3	250	2	Q8RPW3	Q8RPW3 bacillus ce
21	1199	91.2	250	2	Q8KTW7	Q8KTW7 bacillus th
22	315	24.0	263	2	Q8VPD5	Q8VPD5 agrobacteri
23	312	23.7	263	16	Q8UKH0	Q8UKH0 agrobacteri
24	299.5	22.8	268	16	Q88B9	Q88B9 rhizobium l
25	299	22.7	256	2	Q9WMD3	Q9WMD3 agrobacteri
26	260	19.8	269	17	Q97Y13	Q97Y13 sulfolobus
27	256.5	19.5	253	2	Q8KXV8	Q8KXV8 rhizobium e
28	252	19.2	219	2	Q9RH58	Q9RH58 bradyrhizob
29	251	19.1	301	17	Q9HQ42	Q9HQ42 halobacteri
30	242.5	18.4	262	17	Q28763	Q28763 archaeoglob
31	239.5	18.2	271	17	Q978V7	Q978V7 thermoplasm
32	236	17.9	271	16	Q9RXY2	Q9RXY2 deinococcus
33	233.5	17.8	276	16	Q8U664	Q8U664 agrobacteri
34	210	16.0	279	16	Q9PDL8	Q9PDL8 xylella fas
35	195	14.8	136	16	Q8XS86	Q8XS86 ralstonia s
36	192.5	14.6	328	17	Q97CB9	Q97CB9 thermoplasm
37	188	14.3	285	16	Q8F9T6	Q8F9T6 leptospira
38	186	14.1	253	16	Q9RTE2	Q9RTE2 deinococcus
39	185.5	14.1	261	17	Q9HLW9	Q9HLW9 thermoplasm
40	185.5	14.1	280	16	Q8NW27	Q8NW27 staphylococ
41	183.5	14.0	280	16	Q99TB7	Q99TB7 staphylococ
42	181.5	13.8	331	2	Q9ALW1	Q9ALW1 plesiomonas
43	178.5	13.6	326	16	Q92RT6	Q92RT6 rhizobium m
44	176.5	13.4	321	16	Q8P8H8	Q8P8H8 xanthomonas
45	174.5	13.3	341	2	Q93SP1	Q93SP1 plesiomonas

ALIGNMENTS

RESULT 1

Q9L8R8 ID Q9L8R8 PRELIMINARY; PRT; 250 AA.
AC Q9L8R8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative metallohydrolase.
GN AIIA.
OS Bacillus sp. 240B1.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=118641;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=240B1,
RX MEDLINE=20202669; PubMed=10716724;
RA Dong Y.H., Xu J.L., Li X.Z., Zhang L.H.;
RT "AIIA, an enzyme that inactivates the acylhomoserine lactone quorum-
sensing signal and attenuates the virulence of *Erwinia carotovora*.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:3526-3531(2000).
DR EMBL; AF196486; AAF62398.1; -;
DR InterPro; IPR001279; Bactmase-like.
DR Pfam; PF00753; lactamase_B; 1.
KW Hydrolase.
SQ SEQUENCE 250 AA; 28037 MW; 6E5D32E1E8818272 CRC64;

Query Match 100.0%; Score 1315; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 5.9e-105;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVKLYFVPAGRCMLDHSVNSTLTPGELLDLPVWCYLLLETEEGPILVDVTGMPESAVNN 60

Db 1 MTVKLYFVPAGRCMLDHSVNSTLTPGELLDLPVWCYLLLETEEGPILVDVTGMPESAVNN 60

QY 61 EGLFNGTFFVEGQVLPKMTTEEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120

Db 61 EGLFNGTFFVEGQVLPKMTTEEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120

QY 121 IIVQRAEYEAQHSEBYLKECILPNLNKYIIEGDEVYVPGVQLLHTFGHTPGHQSLLIET 180

```
Db 121 IIIVQRAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQLLHTPGHTPGHQSLLIET 180
QY 181 EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
Db 181 EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
QY 241 RGCKVPEPEYI 250
Db 241 RGCKVPEPEYI 250

RESULT 2
Q8KWS6 PRELIMINARY; PRT; 250 AA.
AC Q8KWS6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE AIIA.
GN AIIA.
OS Bacillus sp. A24.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=177211;
RN SEQUENCE FROM N.A.
RC STRAIN=A24;
RX MEDLINE=219320276; PubMed=11932439;
RA Reimann C., Ginot N., Michel L., Keel C., Michaux P.,
RA Krishnapillai V., Zala M., Heurlier K., Triandafillu K., Harms H.,
RA Defago G., Haas D.;
RT "Genetically programmed autoinducer destruction reduces virulence gene
RT expression and swarming motility in Pseudomonas aeruginosa PAO1.";
RL Microbiology 148:923-932(2002).
DR EMBL: AF397400; AAM61772.1; -.
DR InterPro: IPR001279; Blactmase-like.
DR Pfam: PF00753; lactamase_B; 1.
SQ SEQUENCE 250 AA; 28010 MW; 604CF49ABBE2C386 CRC64;

Query Match 97.3%; Score 1280; DB 2; Length 250;
Best Local Similarity 97.2%; Pred. No. 6e-102;
Matches 243; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTVKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLETEEGPILVDTGMPESAVNN 60
Db 1 MTVKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLETEEGPILVDTGMPESAVNN 60
QY 61 EGLFNGTFVEGQVLPKMTEDRIVNIIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
Db 61 EGLFNGTFVEGQVLPKMTEDRIVNIIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
QY 121 IIIVQRAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQLLHTPGHTPGHQSLLIET 180
Db 121 IIIVQRAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQLLHTPGHTPGHQSLLIET 180
QY 181 EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
Db 181 EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
QY 241 RGCKVPEPEYI 250
Db 241 RGCKVPEPEYI 250

RESULT 4
Q8KWN1 PRELIMINARY; PRT; 250 AA.
AC Q8KWN1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE N-acylhomoserine lactone lactonase.
GN AII2.
OS uncultured Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=83428;
RN SEQUENCE FROM N.A.
RA Fray R.G., Dessaux Y.;
RT "Isolation of HSL lactonases and comparison of their activity against
RT various N-acylhomoserine lactone targets.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ505742; CAD44268.1; -.
DR InterPro: IPR001279; Blactmase-like.
DR Pfam: PF00753; lactamase_B; 1.
SQ SEQUENCE 250 AA; 28175 MW; E045D41BDAA659EA CRC64;

Query Match 95.5%; Score 1256; DB 2; Length 250;
Best Local Similarity 95.2%; Pred. No. 7e-100;
Matches 238; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MTVKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLETEEGPILVDTGMPESAVNN 60
Db 1 MTVKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLETEEGPILVDTGMPESAVNN 60
QY 61 EGLFNGTFVEGQVLPKMTEDRIVNIIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
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Db 121 IIIVQRAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQLLHTPGHTPGHQSLLIET 180
QY 181 EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
Db 181 EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
QY 241 RGCKVPEPEYI 250
Db 241 RGCKVPEPEYI 250

RESULT 2
Q8KWS6 PRELIMINARY; PRT; 250 AA.
AC Q8KWS6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE AIIA.
GN AIIA.
OS Bacillus sp. A24.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=177211;
RN SEQUENCE FROM N.A.
RC STRAIN=A24;
RX MEDLINE=219320276; PubMed=11932439;
RA Reimann C., Ginot N., Michel L., Keel C., Michaux P.,
RA Krishnapillai V., Zala M., Heurlier K., Triandafillu K., Harms H.,
RA Defago G., Haas D.;
RT "Genetically programmed autoinducer destruction reduces virulence gene
RT expression and swarming motility in Pseudomonas aeruginosa PAO1.";
RL Microbiology 148:923-932(2002).
DR EMBL: AF397400; AAM61772.1; -.
DR InterPro: IPR001279; Blactmase-like.
DR Pfam: PF00753; lactamase_B; 1.
SQ SEQUENCE 250 AA; 28010 MW; 604CF49ABBE2C386 CRC64;

Query Match 97.3%; Score 1280; DB 2; Length 250;
Best Local Similarity 97.2%; Pred. No. 6e-102;
Matches 243; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTVKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLETEEGPILVDTGMPESAVNN 60
Db 1 MTVKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLETEEGPILVDTGMPESAVNN 60
QY 61 EGLFNGTFVEGQVLPKMTEDRIVNIIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
Db 61 EGLFNGTFVEGQVLPKMTEDRIVNIIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
QY 121 IIIVQRAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQLLHTPGHTPGHQSLLIET 180
Db 121 IIIVQRAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQLLHTPGHTPGHQSLLIET 180
QY 181 EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
Db 181 EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
QY 241 RGCKVPEPEYI 250
Db 241 RGCKVPEPEYI 250

RESULT 3
Q8KTW5 PRELIMINARY; PRT; 250 AA.
AC Q8KTW5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE AIIA-like protein.
GN AIIA.
```


RT Widespread in Many Subspecies of *Bacillus thuringiensis*.;
 RL Appl. Environ. Microbiol. 68:3919-3924(2002).
 DR EMBL; AF478054; AAM92135.1; -.
 DR InterPro; IPR001279; Blactmase-like.
 DR Pfam; PF00753; lactamase B; 1.
 SQ SEQUENCE 250 AA; 28163 MW; BA2D7F09CF3F39DD CRC64;

Query Match 92.9%; Score 1222; DB 2; Length 250;
 Best Local Similarity 91.2%; Pred. No. 5.8e-97;
 Matches 228; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MTVKLYFVPAAGRCMLDHSVSNSTLTGCELLDLPWCYLLTEEGPILVDTGMPESAVNN 60
 Db 1 MTVKLYFIPAGRCMLDHSVSNSTLTGCKLNLFPWCYLLTEEGPILVDTGMPESAVNN 60
 Qy 61 EGLFNGTFVEGQILPKMTEEDRIWNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 Db 61 EGLFNGTFVEGQILPKMTEEDRIWNILKRVGYDPEDLLYIISSHLHFDHAGNGAFINTP 120
 Qy 121 IIVQRAEYEAQHSEYLYKECILPNLNKYIIEGDEYVVPVGVQLLTPGHTPGHOSLLIET 180
 Db 121 IIVQTEYEAALHREYMKECILPHLNKYIIEGDEYVVPVGVQLLTPGHSFGHOSLFIET 180
 Qy 181 EKSGPVLLTTIDASTYKTNFENVPFAGFDSALSSIKRLKEVVMKPKPIVFFFGHDIEQE 240
 Db 181 EQSGVLLTTIDASTYKTNFENVPFAGFDPALSSIKRLKEVVMKPKPIVFFFGHDIEQE 240
 Qy 241 RGCKVFPEYI 250
 Db 241 KGCRVFPEYI 250

RESULT 11

Q8KWT3 PRELIMINARY; PRT; 250 AA.

ID Q8KWT3
 AC Q8KWT3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE AIIA-like protein.
 GN AIIA.
 OS *Bacillus cereus*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IBN35;
 RX MEDLINE=22142036; PubMed=12147491;
 RA Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
 PT "Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
 RT Widespread in Many Subspecies of *Bacillus thuringiensis*.";
 RL Appl. Environ. Microbiol. 68:3919-3924(2002).
 DR EMBL; AF478051; AAM92142.1; -.
 DR InterPro; IPR001279; Blactmase-like.
 DR Pfam; PF00753; lactamase B; 1.
 SQ SEQUENCE 250 AA; 28113 MW; DFF28F553BA07C2E CRC64;

Query Match 92.8%; Score 1220; DB 2; Length 250;
 Best Local Similarity 91.2%; Pred. No. 8.6e-97;
 Matches 228; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MTVKLYFVPAAGRCMLDHSVSNSTLTGCELLDLPWCYLLTEEGPILVDTGMPESAVNN 60
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 Qy 61 EGLFNGTFVEGQILPKMTEEDRIWNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 Db 61 EGLFNGTFVEGQILPKMTEEDRIWNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 Qy 121 IIVQRAEYEAQHSEYLYKECILPNLNKYIIEGDEYVVPVGVQLLTPGHTPGHOSLLIET 180
 Db 121 IIVQTEYEAALHREYMKECILPHLNKYIIEGDEYVVPVGVQLLTPGHSFGHOSLFIET 180

Qy 181 EKSGPVLLTTIDASTYKTNFENVPFAGFDSALSSIKRLKEVVMKPKPIVFFFGHDIEQE 240
 Db 181 EQSGVLLTTIDASTYKTNFENVPFAGFDPALSSIKRLKEVVMKPKPIVFFFGHDIEQE 240
 Qy 241 RGCKVFPEYI 250
 Db 241 KGCRVFPEYI 250

RESULT 12

Q8RPW9 PRELIMINARY; PRT; 250 AA.

ID Q8RPW9
 AC Q8RPW9;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE AHL-lactonase.
 GN AIIA-COT1.
 OS *Bacillus sp. COT1*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=176903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COT1;
 RX MEDLINE=21914084; PubMed=11916693;
 RA Dong Y.H., Gusti A.R., Zhang Q., Xu J.L., Zhang L.H.;
 RT "Identification of Quorum-Quenching N-Acyl Homoserine Lactonases from
 RL *Bacillus* Species.";
 DR Appl. Environ. Microbiol. 68:1754-1759(2002).
 DR EMBL; AF350927; AAL98716.1; -.
 DR InterPro; IPR001279; Blactmase-like.
 DR Pfam; PF00753; lactamase B; 1.
 SQ SEQUENCE 250 AA; 28084 MW; 3508246790F50709 CRC64;

Query Match 92.7%; Score 1219; DB 2; Length 250;
 Best Local Similarity 91.2%; Pred. No. 1.1e-96;
 Matches 228; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MTVKLYFVPAAGRCMLDHSVSNSTLTGCELLDLPWCYLLTEEGPILVDTGMPESAVNN 60
 Db 1 MTVKLYFVPAAGRCMLDHSVSNSTLTGCKLNLFPWCYLLTEEGPILVDTGMPESAVNN 60
 Qy 61 EGLFNGTFVEGQILPKMTEEDRIWNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 Db 61 ENLFEFTFAGQILPKMTEEDRIAILKRAYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 Qy 121 IIVQRAEYEAQHSEYLYKECILPNLNKYIIEGDEYVVPVGVQLLTPGHTPGHOSLLIET 180
 Db 121 IIVQRAEYEAQHSEYLYKECILPNLNKYIIEGDEYVVPVGVQLLTPGHSFGHOSLLIET 180
 Qy 181 EKSGPVLLTTIDASTYKTNFENVPFAGFDSALSSIKRLKEVVMKPKPIVFFFGHDIEQE 240
 Db 181 EKSGVLLTTIDASTYKTNFENVPFAGFDPALSSIKRLKEVVMKPKPIVFFFGHDIEQE 240
 Qy 241 RGCKVFPEYI 250
 Db 241 KGCKVFPEYI 250

RESULT 13

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ID Q8KTX1
 AC Q8KTX1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE AIIA-like protein.
 GN AIIA.
 OS *Bacillus thuringiensis* serovar canadensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=180855;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN=HD224;
RX MEDLINE=22142036; PubMed=12147491;
RA Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
RT "Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
RT Widespread in Many Subspecies of Bacillus thuringiensis.";
RL Appl. Environ. Microbiol. 68:3919-3924(2002).
DR EMBL; AF478047; AA92128.1; -.
DR InterPro; IPR001279; Blactmase-like.
DR Pfam; PF00753; lactamase_B; 1.
SQ SEQUENCE 250 AA; 28003 MW; 6EB53AF4A152B244 CRC64;

Query Match 92.5%; Score 1216; DB 2; Length 250;
Best Local Similarity 91.2%; Pred. No. 1.9e-96;
Matches 228; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

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Db 1 MTVKLYFVPAGRCMLDSSVNSTLTPGELLDFVWCYLLETEEGPILVDTGMPESAVNN 60
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Db 61 EGLFNGTFFVGGVLPKMTTEEDRVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
QY 121 IIIVQAEYEAQAHSSEYKCEILPNLNKYKIEGDYEVVPGVQLLHTPGHSPGHSLFIET 180
Db 121 IIIVQAEYEAQAHSSEYKCEILPNLNKYKIEGDYEVVPGVQLLHTPGHSPGHSLFIET 180
QY 181 EKSGPVLLTIDASYTKENFENVPFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
Db 181 EKSGPVLLTIDASYTKENFENVPFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
QY 241 RGCKVPPEYI 250
Db 241 KGCRVPPEYI 250

RESULT 14
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AC Q8RPW7;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE AHL-lactonase (Aila-like protein).
GN Aila-B2 OR Aila.
OS Bacillus thuringiensis,
OS Bacillus thuringiensis (subsp. aizawai),
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis serovar indiana.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1426, 1433, 29339, 160850;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.thuringiensis; STRAIN=B2;
RX MEDLINE=21914084; PubMed=11916693;
RA Dong Y.H., Gusti A.R., Zhang Q., Xu J.L., Zhang L.H.;
RT "Identification of Quorum-Quenching N-Acyl Homoserine Lactonases from
RT Bacillus Species.";
RL Appl. Environ. Microbiol. 68:1754-1759(2002).
DR EMBL; AF350934; AAL98723.1; -.
DR InterPro; IPR001279; Blactmase-like.
DR Pfam; PF00753; lactamase_B; 1.
SQ SEQUENCE 250 AA; 28004 MW; 6055D4F4A152B244 CRC64;

Query Match 92.2%; Score 1212; DB 2; Length 250;
Best Local Similarity 90.8%; Pred. No. 4.2e-96;
Matches 227; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

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Db 1 MTVKLYFVPAGRCMLDSSVNSTLTPGELLDFVWCYLLETEEGPILVDTGMPESAVNN 60
QY 61 EGLFNGTFFVGGVLPKMTTEEDRVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
Db 61 EGLFNGTFFVGGVLPKMTTEEDRVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
QY 121 IIIVQAEYEAQAHSSEYKCEILPNLNKYKIEGDYEVVPGVQLLHTPGHSPGHSLFIET 180
Db 121 IIIVQAEYEAQAHSSEYKCEILPNLNKYKIEGDYEVVPGVQLLHTPGHSPGHSLFIET 180
QY 181 EKSGPVLLTIDASYTKENFENVPFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
Db 181 EKSGPVLLTIDASYTKENFENVPFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
QY 241 RGCKVPPEYI 250
Db 241 KGCRVPPEYI 250

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AC Q8RJA0;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE AHL-lactonase.
GN Aila-B20 OR Aila-B22.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B20, and B22;
RX MEDLINE=21914084; PubMed=11916693;
RA Dong Y.H., Gusti A.R., Zhang Q., Xu J.L., Zhang L.H.;
RT "Identification of Quorum-Quenching N-Acyl Homoserine Lactonases from
RT Bacillus Species.";
RL Appl. Environ. Microbiol. 68:1754-1759(2002).
DR EMBL; AF350932; AAL98721.1; -.
DR EMBL; AF350934; AAL98723.1; -.
DR InterPro; IPR001279; Blactmase-like.
DR Pfam; PF00753; lactamase_B; 1.
SQ SEQUENCE 250 AA; 28004 MW; 6055D4F4A152B244 CRC64;

Query Match 92.2%; Score 1212; DB 2; Length 250;
Best Local Similarity 90.8%; Pred. No. 4.2e-96;
Matches 227; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTVKLYFVPAGRCMLDSSVNSTLTPGELLDFVWCYLLETEEGPILVDTGMPESAVNN 60
Db 1 MTVKLYFVPAGRCMLDSSVNSTLTPGELLDFVWCYLLETEEGPILVDTGMPESAVNN 60
QY 61 EGLFNGTFFVGGVLPKMTTEEDRVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
Db 61 EGLFNGTFFVGGVLPKMTTEEDRVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
QY 121 IIIVQAEYEAQAHSSEYKCEILPNLNKYKIEGDYEVVPGVQLLHTPGHSPGHSLFIET 180
Db 121 IIIVQAEYEAQAHSSEYKCEILPNLNKYKIEGDYEVVPGVQLLHTPGHSPGHSLFIET 180
QY 181 EKSGPVLLTIDASYTKENFENVPFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
Db 181 EKSGPVLLTIDASYTKENFENVPFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
QY 241 RGCKVPPEYI 250
Db 241 KGCRVPPEYI 250

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Qy 241 RGCKVFPEYI 250
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Db 241 KGCRVFPEYI 250

Search completed: February 20, 2004, 16:26:00
Job time : 36 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 02:25:33 ; Search time 2464 Seconds

(without alignments)
14809.896 Million cell updates/sec

Title: US-10-019-661-1

Perfect score: 1222

Sequence: 1 ctttactgtattgtttatt.....tcatttgggtctctttgagt 1222

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	75.8	6.2	1101	29	CNS0039G
2	74	6.1	576	29	CNS035N7
c 3	72.2	5.9	1165	13	AL228940 Tetraodon
4	72	5.9	1124	13	BX338369 BX338369
					BX436282 BX436282

5	58.6	5.6	1123	14	CD325190
c 6	67.6	5.5	1067	14	CD386564
7	67	5.5	1101	29	CNS0039G
c 8	67	5.5	1201	9	AL565455
c 9	66.8	5.5	1101	29	CNS00EVL
10	66.8	5.5	1201	13	BX335216
11	66.4	5.4	897	29	CNS07ABZ
c 12	66.4	5.4	1056	13	EX415058
c 13	66.2	5.4	1201	13	BX395112
c 14	66	5.4	981	13	BX425658
15	65.8	5.4	1200	13	BX436510
c 16	65.6	5.4	1201	13	BX357882
c 17	65.4	5.4	991	14	CD248081
c 18	64.8	5.3	1200	13	EX437758
19	64.4	5.3	739	14	CF217629
20	64.4	5.3	1101	29	CNS00EVL
21	64.4	5.3	1309	10	BE420736
c 22	63.8	5.2	1101	29	CNS003B4
c 23	63.4	5.2	1048	13	EX456942
24	63.2	5.2	1044	13	EX415231
25	63.2	5.2	1101	29	CNS001FB
26	62.8	5.1	756	28	AZ192623
27	62.8	5.1	974	29	CNS00ITT
c 28	62.6	5.1	1101	29	CNS002LJ
29	62.6	5.1	1128	13	BX337294
c 30	62.4	5.1	1126	13	EX446388
c 31	62.2	5.1	1184	29	CNS04P4P
c 32	62.2	5.1	1201	9	AL547503
33	62	5.1	1287	29	CG753143
34	61.6	5.0	922	28	AZ548363
c 35	61.4	5.0	1101	29	CNS003B0
36	61.2	5.0	717	29	CNS06ZNC
37	61.2	5.0	932	9	AL514901
c 38	61.2	5.0	953	13	BX331505
c 39	61.2	5.0	994	13	BX414650
c 40	61.2	5.0	1002	14	CD389396
c 41	61.2	5.0	1101	29	CNS00Z6Z
c 42	61.2	5.0	1159	13	BX341161
c 43	61	5.0	920	29	CNS01UQL
c 44	60.8	5.0	961	28	AZ691838
c 45	60.8	5.0	1101	29	CNS00LJT

ALIGNMENTS

RESULT 1
CNS0039G/c

LOCUS

DEFINITION

CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL063921.1 GI:4941778
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)

Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osogawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <http://bacpac.med.buffalo.edu/drosophila.bac.htm>.

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FEATURES
source
Location/Qualifiers
1. .1101
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279 GACTGAAGAAGATAGAAATCGTGAATATTTTAAACGGGTGGTTATGTAGCCGGAAGACCT 338

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QY 399 AATATACCAATCATTTGACAGCGTGTGAATATGAGCGGCGGAGCATAGCGAAGATA 458

DB GAGGKDDGNGKRAHDDDDIDGIRKDDDDKRAKDDDMKRAKSTWSDAAWAKKELERWWWKNDK 518

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[illegible]

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Db      676 DRDAAWADA...TTTDTDDDDKRRRKGARRRRRTARAADWWTWKAWDKAKDW 617
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D6
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QY 759 AGAGCAGGAAAGGGGATGTAAAGTGTTCCTCGAATATATATATAGTACAAAAGTCATGAGC 818

DB	536	TTATTCGCTCATGACTTTTTCGTTTAAATGATTTTTTAAATAAGTTATAAACTTTTAA 878
QY	819	TTATTCGCTCATGACTTTTTCGTTTAAATGATTTTTTAAATAAGTTATAAACTTTTAA 878

[illegible]

Ddb

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939 GCAATCATCACTTCGTTACTGTGATGGTCAACTACCCATANGAAATATTTTTTAAAGTC 998

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RESULT 2	CNS035N7	576 bp	DNA	linear	GSS 01-SEP-2000
LOCUS	Tetraodon nigroviridis genome survey sequence pUC-Ori end of clone				
DEFINITION	214A06 of library G from Tetraodon nigroviridis, genomic survey sequence.				

ACCESSION	AL228940
VERSION	AL228940.1
KEYWORDS	GSS; genome survey sequence.
SOURCE	Tetradodon nigroviridis
ORGANISM	Tetradodon nigroviridis

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

1
REFERENCE
AUTHORS
Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fixames, C., Wincker, P., Brottier, P., Quetier, F.,

TITLE Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence

JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PubMed 10835645

2
REFERENCE
AUTHORS
Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,

TITLE Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater buefferfish *Tetraodon nigroviridis*

JOURNAL
MEDLINE
Genome Res. 10 (7), 939-949 (2000)
20359837
PURMED
10899143

REFERENCE
3 (bases 1 to 576)
Genoscope.
AUTHORS
Direct Submission
TITLE

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-sequencing project of the *Tetrahodon nigroviridis* genome. For more information, please take a look at

FEATURES
 source 1..576
 Location/Qualifiers
<http://www.genoscope.cns.fr/Tetraodon>.

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/db_xref="taxon:99883"

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/clone="214A06"
/clone lib="G"
/note="Genoscope sequence ID : C0AG214BA03SP1-end :

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ORIGIN
PUC-Orl¹¹

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Gaps	0;		

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Db	12	TTTTTTTTTTTGGAWTTTTCGATTTCGAAAAAATAAATAATAGATAATTAAGATTTTAAATAAA	71
Ov	797	TATAGTACAAAAAGCTCATGAGCTTATTTCGCTCATGACTTTTTCGTTTAAATGATTTTTTTT	856

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Jamie Thompson, University of WI
 cDNA Library Preparation: Gina Zastrow-Hayes
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
 Plate: NDKM74 row: e column: 02
 High quality sequence start: 8
 High quality sequence stop: 462.
FEATURES Location/Qualifiers
 source
 1. 1067
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic trophoblasts, made from WA01 stem
 cells"
 /lab_hosts="DH10B TonA"
 /clone_lib="NIH MGC 173"
 /note="vector: pDONR201; Site 1: attP2; Site 2: attP1;
 LIBR PRIMING - oligo dT; METHOD - full-length enriched;
 LIBR PROVIDER - Bradfield"

ORIGIN
 Query Match 5.5%; Score 67.6; DB 14; Length 1067;
 Best Local Similarity 43.6%; Pred. No. 0.0011;
 Matches 265; Conservative 0; Mismatches 338; Indels 5; Gaps 1;
 582 TGACACAGAAAAATCCGGTCCTGATTATTAAACGATTGATCGATCGTATACGAAAGAGAA 641
 926 TTAATATATAATATTTTAAATTTTATTTTAAATTTATATAAATTTTAAATATTA 867
 642 TTTTGAATAAGTGCATTTGCGGGATTGATTCAGAAATAGCTTTATCTCAATTA 701
 866 TGATATANNTTAAATTTTNNAAATTTTAAATTAANAATAAATTTTNTATATA 807
 702 ACGTTTAAAGAGTGTGATGAAGAGAGACCGGATTTCTTTGTCGACATGATAGA 761
 806 TAATATTATATAATTTTATTTANTTNATTTTAAATTTATTTTAAATATAAATAA 747
 762 GCAGGAAAGGGGATGTAAGTGTCCCTGATATATATAGTACAAAAGTCATGAGCTTA 821
 746 ANANAAAAAATAAATAATTTTATTTATTTTAAATAAATAAATAATTTTAAAA 687
 822 TTCGCTCATGACTTTTTCGTTTAAATGATTTTAAATAGTTTATAAACTTTTAA 881
 686 TAATTAATAAATAATATATTTTATTTTANATTATAATAATAATAATAATTTTATT 627
 882 CTATCTTCATTT-----AATTGATAGTACGTAAAGTTTACATCATAGGAGTATCTGTT 936
 626 TTAATTTNANNTTTATAAATTTATTTTATATAAAAAAATAAATAAATAATTTTAT 567
 937 GAGCAATCATCACTTCGTTACTGTGATGGTCAACTACCCATATCAAAATTTTATAAG 996
 566 AATAATAAAAAAATTTATTTTNNAAAAAANNNNNNNNNNTTTTATTTTAAAAA 507
 997 TCCCATCTCGAAAGTAAATCCACATATCACAGTCTATTAAATCTGATCCTTCTCATCTA 1056
 506 TTTNNCTCTTTNTTTTAAAAAANNNNNNNNNNTTTTATTTTATTTTATTTT 447
 1057 ATGTTAAATTTTCCTTTTCGGCGGTATCCATACGTGTAATGAATGTTTAAATTCATCTG 1116
 446 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 387
 1117 TTTTGTGAGAAAGATATCTCTTTTTCGTTTAAATTTGACTCGACATGATATCTTTATTT 1176

Db 386 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 327
Qy 1177 CTGTGTTT 1184
Db 326 TTTTATTTT 319
RESULT 7
LOCUS CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
ACCESSION AL063921
VERSION AL063921.1 GI:4941778
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammeter in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR08K10"
 /clone_lib="RPCI-98"
 /note="end : TET3"

ORIGIN

Query Match 5.5%; Score 67; DB 29; Length 1101;
 Best Local Similarity 19.8%; Pred. No. 0.0015;
 Matches 110; Conservative 221; Mismatches 234; Indels 0; Gaps 0;
Qy 628 TATACGAAAGAGAAATTTTGAAATGAAGTCCCATTTGCGGGATTTCAGTAATTAGCT 687
Db 397 TATAWAWWWTTTTTTTAAWAAWAAATAATTTWAAWAAWAAATAATTTWAAWAAAA 456
Qy 688 TTATCTTCAATTAACGTTTAAAAGAGTGGTGATGAAGAGAGCGGATTTGTTCTTT 747
Db 457 WAWTAWTTTATWAAAAAATAAATTTTATTTTATTTTATTTTATTTTATTTTAA 516
Qy 748 GGACATGATATACAGCAGGAAGGGATGTAAAGTGTTCCTCGAATATATATAGTACAA 807
Db 517 WAAAAAATAAATAAATAAATAAATAATTTTAAWAAWAAWAAWAAWAAWAAWAAW 576
Qy 808 AAGTCATGACTTATTCGCTCATGACTTTTCGTTTAAATGATTTTAAATAGTTAT 867
Db 577 TTYHYTYTYTYTYTYTYHYHYTYHYHYTYHYHYTYHYHYTYHYHYTYHYHYHYTY 636

QY	868	AAACTTTTGTAGACATCTCTCAATTAATTAGTACGTAAGGTTTACATCATAGGAG	927
Db	637	AYYYYYTTCMYHHYHHHAAHAAWTTTTHWTHAVHWATYHHYHHYMYCAMCMWTH	696
QY	928	TATCTTGTTCGACCAATCTCTGCTTACTGTGATGCTCAATACCACATATCAATAT	987
Db	697	TCHCYHHYHHYTAHHHTHHYHHYHHYHHYHHYHHYHHYHHYHHYHHYHHYHHY	756
QY	988	TTTTATAAGTCCCATCTCTCGAAAGTAATCCACATATCACATGCTATTAATCGATCCT	1047
Db	757	WYAAHAMMMHHHAAHAAWAAWTTTHHHYHHYHHYHHYHHYHHYHHYHHYHHY	816
QY	1048	CTTCATCTAATGTAATTTCTTTTTCGGGATCCATCTGTTAAATGAACTGTTTAA	1107
Db	817	HYHTATCTWTHHHMMTTHWYHHHTHHWHTTTHWAAWHHTHWCWWHHATTTWTHAHC	876
QY	1108	ATTCATCTGTTTGTGAGAAAGATATCTTTTGTGTTTAAATGACTCGACATGATAT	1167
Db	877	WACMTWMMHMMHHHMMHACHHHHTHMMCHHHHMECTCHHHHTMYHHMTCHWMMHMH	936
QY	1168	CTTTTATTTCTGTTTTCCTAAAAA	1192
Db	937	WHHMMATWTTTMMCMCMH	961
RESULT 8			
AL565455/c			
LOCUS			
DEFINITION	AL565455 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone	1201 bp	linear EST 12-MAY-2003
ACCESSION	CS0DF005YO18	3-PRIME, mRNA	sequence.
VERSION	AL565455		
KEYWORDS	AL565455.2	GI:30549492	
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	1. (bases 1 to 1201)		
COMMENT	Li, W.B., Gruber, C., Jesse, J., and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001) On Feb 16, 2001 this sequence version replaced gi:12916848. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9232.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DF005BH09NP1&cluster=9232.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DF005BH09NP1.		
FEATURES			
source	Location/Qualifiers		
	1. .1201		
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	/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."		
ORIGIN			
Query Match	5.5%;	Score 67;	DB 9; Length 1201;
Best Local Similarity	31.8%;	Pred. No. 0.0015;	
Matches	235;	Conservative 112;	Mismatches 392; Indels 0; Gaps 0;

QY	456	ATATTTGAAGAAGTATATTCGCGAATTTAAACTACAAAATCAATGAAGGTGATTATGA	515
Db	1185	ATWTATWTATWTATATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWT	1126
QY	516	AGTCGTACACGAGGAGTTCATATTTGCAATACACAGGCCCATCTCCAGGGGCAATCAATCGCT	575
Db	1125	ATWTATWTATWTATATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWT	1066
QY	576	ATTAAATGAGACAGAAAAATCCGGTCTGTATTTAATTAACGATTGATCGATACGATACGAA	635
Db	1065	ATWTATWTATWTATATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWT	1006
QY	636	AGAGAATTTTGAATAAGCAAGTGCATTTGCGGATTTGATTCAGAAATAGCTTTATCTTC	695
Db	1005	ATWTATWTATWTATATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWT	946
QY	696	AATTAACGTTTAAAAAGAGTGTGATGAAGAAGAGCCGATTTGTTCTTTTGGACATGA	755
Db	945	ATWTATWTATWTATATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWT	886
QY	756	TATAGACGAGGAAGGGGATGAAGTGTTCCTGATATATATATATATATATATATATATAT	815
Db	885	ATWTATWTATWTATATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWT	826
QY	816	AGCTTATTCGCTCATGACTTTTTCGTTTAAATGATTTTTTAAATAAGTTATATAACCTTT	875
Db	825	ATWTATWTATWTATATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWT	766
QY	876	TTAGAACTATCTTCATTTAAATGATAGTAGTAAAGGTTTACATCATTTAGGAGTATCTTGT	935
Db	765	ATWTATWTATWTATATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWT	706
QY	936	TGACCAATCATCTTCGTTACTGTGATGTGCACTACCCATCCATGAAATATTTTATATAA	995
Db	705	ATWTATWTATWTATATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWT	646
QY	996	GTCCCATCTTCGAAAGTAATCCACATATCACAGTCTATTAATCTGATCTCTTCTCATCT	1055
Db	645	ATWTATWTATWTATATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWT	586
QY	1056	AATGTTAAATTTCTTTTGGGGGATCCATCTGTTAAATGAAGTGTGTTTAAATCATCT	1115
Db	585	ATWTATWTATWTATATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWT	526
QY	1116	GTTTTGTGAGAAAGATATCTTTTGTGTTTAAATGCTGACTCGACATGATATCTTTTATT	1175
Db	525	ATWTATWTATWTATATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWT	466
QY	1176	TCTTGTGTTTCTCTAAAAAGA	1194
Db	465	ATWTATWTATWTATATWTA	447
RESULT 9			
CNS00EVL			
LOCUS			
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC:	1101 bp	DNA linear GSS 04-JUN-1999
	BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit		
	fly), genomic survey sequence.		
ACCESSION	AL069706		
VERSION	AL069706.1	GI:4949849	
KEYWORDS	GSS.		
SOURCE	Drosophila melanogaster (fruit fly)		
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
	Ephyroidea; Drosophilidae; Drosophila.		
REFERENCE	1. (bases 1 to 1101)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :		
	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		

[illegible]

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y      999 CCACTCTGGAAGTAATCCACATATCACAGTCTATTAATCAATCGATCTCTTCACTAA 1058
b      498 ATTATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 557
y      1059 GTTAATTTTCTTTTTTGGCGGTATCCATCTGTTAAATGAATGTTTTTAATCACTGTT 1118
b      558 TTTWATTTTTTTTTTTTTTTTTTATTTTTTTTTTTTTTTTTTTTTTTTAAATATTTT 617
y      1119 TTGTGAGAAAGATACTCTTTTTTGGTTTTTAATTCGACTCGACATGATATCTTTATTTCT 1178

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y		1179 TGTTCCTTAAAAAGACAGGGGCTCATTT	1208
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x415058/c		BX415058 Homo sapiens THYMUS	cDNA clone CSOCAP004YG19
OCCUR		3-PRIME, mRNA sequence.	
DEFINITION		BX415058	
CCESSION		BX415058	
VERSION		BX415058.1 GI:30767520	
EYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	

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REFERENCE
1 (bases 1 to 1056)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0CAP004AD10NP1.
Location/Qualifiers
1..1056
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/mol_type="mRNA"
FEATURES
source

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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned, into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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Best Local Similarity 36.8%; Pred. No. 0.002;

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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 5.4%; Score 66; DB 13; Length 981;
Best Local Similarity 32.9%; Pred. No. 0.0024;
Matches 158; Conservative 90; Mismatches 232; Indels 0; Gaps 0;
QY 705 TTTAAAGAGTGGTGGTGAAGAGAGAGCGAGTTGTTCTTTGGACATGATATAGACGA 764
DB 675 TDAAWRRARARAGGGGGGGGGGGTGTWTKKTKKKKKKKGGGRRGRGGGGGR 616
QY 765 GGAAGGGGATGAAGTGTCCCTGAAATATATAGTACAAAAGTCATGAGCTTATTC 824
DB 615 GKRRADGRARRRRAARGDKKKKAAAAAAXKKKKKDRARAWKTKTDRAPAAARAG 556
QY 825 GCTCATGACTTTTTCGTTTAAAGTATTTTAAATAGTTTATAAAGTATTAAGACTA 884
DB 555 GAGRGGGAGAGDWKKKKKARRRRGRKKKKKKDTTTTTTTTTTTTTTTIDWGRKKG 496
QY 885 TCCTTCATTAAATGATAGTACGTAAGGTTTACATCATAGGAGTATCTTGTGAGCAATC 944
DB 495 GRGGGAATKTTTAWKTKRRAWKDARRGDWAAMTTTKRAGGARADTTTTTTTTTK 436
QY 945 ATCACTTCGTTAGTGTGATGCTCACTACCCATATGAAATATTTTATTAAGTCCATCC 1004
DB 435 DRRRATKRAAADKDDAAAAAARADRRRAADKKTWTTTTTTTTTTTAKWTWTWT 376
QY 1005 TCGAAGTATCCACATATCACATCTATTAATCTGATCTCTTCACTCAATGTTAAT 1064
DB 375 TTWDGRTTAWAAAAAATTTKTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 316
QY 1065 TTTCTTTTTTGGCGGTATCCACTGTTAATGAAGTGTTTTAAATCATCTGTTTTGTG 1124
DB 315 TT 256
QY 1125 AGAAGATATCTTTTGTGTTTAAATGACTCGACATGATATCTTTATTTCTGTTT 1184
DB 255 TT 196

RESULT 15
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DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX436510
VERSION BX436510.1 GI:30770190
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1200)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5393.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0CAP002AF05QPI&cluster=5393.f. Contact :

Peng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0CAP002AF05QPI.
Location/Qualifiers
1. .1200
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 5.4%; Score 65.8; DB 13; Length 1200;
Best Local Similarity 38.3%; Pred. No. 0.0026;
Matches 230; Conservative 57; Mismatches 308; Indels 5; Gaps 1;
QY 585 GACAGAAAAATCCGGTCTGTATTATTAACGATGATGATCGTATACGAAAGAGATTT 644
DB 421 GACACAGATCCGAGTGTCTGTACCCCTCAAGGATTTARACTTAAACAAAAATCAATAA 480
QY 645 TGAATGAAGTCCCATTTGCGGGATTTGATTGAGATTTAGCTTTATCTTCAATTAACG 704
DB 481 ATAAATGTGAATTTGTCTCTTGTATTTTGGATTTAGRRRTTACTACCTTAAGR 540
QY 705 TTTAAAGAGTGGTGTATGAAAGAGAGCGAGTTTCTTTTGGACATGATATAGACGA 764
DB 541 RRRRRRRRRRAGGGGGGGGGGSAASAAAWTAAAAAASAAAAAASAAAAA 600
QY 765 GGAAGGGGATGTAAGTGTTCCTGAAATATATAGTACAAAAGTCATGAGCTTATTC 824
DB 601 AAAAAAASAAAAAASAAAAAASAAAAAASAAAAAASAAAAAASAAAAA 660
QY 825 GCTCATGACTTTTTCGTTTAAATGATTTTAAATAGTTTATAAAGTATTAAGACTA 884
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QY 885 TCCTTCATTAAATGATAGTACGTAAGGTTTACATCATAGGAGTATCTTGTGAGCAATC 944
DB 721 TANTAAATTTATTTTAAATATAAASAAAWTAAATTTTAAATTTTAAATAAT 780
QY 945 ATCACTTCGTTAGTGTGATGCTCACTACCCATATGAAATATTTTATAGTCCCATCC 1004
DB 781 AAAAAATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 840
QY 1005 TCGAAGTATCCACATATCACATCTATTAATCTGATCTCTTCACTCAATGTTAAT 1064
DB 841 TTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 900
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DB 901 TTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 955
QY 1125 AGAAGATATCTTTTGTGTTTAAATGACTCGACATGATATCTTTATTTCTGTTT 1184
DB 956 TTTTAAATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1015

Search completed: February 24, 2004, 04:22:28
Job time : 2470 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 03:41:17 ; Search time 1437 Seconds
(without alignments)
2977.738 Million cell updates/sec

Title: US-10-019-661-1

Perfect score: 1222

Sequence: 1 ctttactgtattgtttatt.....tcatttgggtctctttgagt 1222

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59.8	4.9	3673778	14	US-10-312-841-2
2	57.8	4.7	673	12	Sequence 2, Appli
3	56	4.6	3673778	14	Sequence 57885, A
4	55.6	4.5	6419	14	Sequence 1, Appli
5	55.6	4.5	14006	14	Sequence 240, App
6	54.8	4.5	516	9	Sequence 1931, Ap
7	54.8	4.5	6109	12	Sequence 5785, Ap
8	54.8	4.5	6109	14	Sequence 33, Appl
9	53.4	4.4	6035	14	Sequence 299, App
10	53.4	4.4	15548	14	Sequence 1497, Ap
11	53.2	4.4	15732	14	Sequence 2128, Ap
12	53.2	4.4	15732	14	Sequence 95, Appl
13	53	4.3	6436	14	Sequence 107, App
14	53	4.3	8776	16	Sequence 654, App
15	52.8	4.3	158001	16	Sequence 150, App
GENERAL INFORMATION					

16	52.6	4.3	9539	14	US-10-239-676-52	Sequence 52, Appl
17	52.6	4.3	9539	14	US-10-240-453-54	Sequence 54, Appl
18	52.6	4.3	11178	12	US-10-221-613-16	Sequence 16, Appl
19	52.4	4.3	446	9	US-09-960-352-3400	Sequence 3400, Ap
20	52.4	4.3	5032	12	US-10-221-613-39	Sequence 39, Appl
21	52.2	4.3	6713	14	US-10-311-455-1053	Sequence 1053, Ap
22	52.2	4.3	6713	14	US-10-240-485-79	Sequence 79, Appl
23	52.2	4.3	10286	14	US-10-239-676-14	Sequence 14, Appl
24	52.2	4.3	10286	14	US-10-240-453-22	Sequence 22, Appl
25	52	4.3	17934	14	US-10-311-455-1692	Sequence 1692, Ap
26	51.8	4.2	5518	14	US-10-311-455-1304	Sequence 1304, Ap
27	51.6	4.2	7597	14	US-10-311-455-986	Sequence 986, App
28	51.4	4.2	7597	14	US-10-311-455-1981	Sequence 1981, Ap
29	51.4	4.2	9539	14	US-10-239-676-51	Sequence 51, Appl
30	51.4	4.2	9539	14	US-10-240-453-53	Sequence 53, Appl
31	51.2	4.2	5127	14	US-10-239-676-132	Sequence 132, App
32	51.2	4.2	6145	14	US-10-311-455-945	Sequence 945, App
33	51.2	4.2	14649	14	US-10-239-676-121	Sequence 121, App
34	51.2	4.2	14649	14	US-10-240-453-141	Sequence 141, App
35	51	4.2	17703	16	US-10-257-166-34	Sequence 34, Appl
36	50.8	4.2	5666	14	US-10-311-455-1746	Sequence 1746, Ap
37	50.8	4.2	7921	14	US-10-311-455-1944	Sequence 1944, Ap
38	50.8	4.2	15674	14	US-10-311-455-336	Sequence 336, App
39	50.8	4.2	15674	14	US-10-240-485-30	Sequence 30, Appl
40	50.6	4.1	6314	14	US-10-240-452-14	Sequence 14, Appl
41	50.4	4.1	5244	16	US-10-257-166-95	Sequence 95, Appl
42	50.4	4.1	7990	14	US-10-311-455-131	Sequence 131, App
43	50.4	4.1	7990	14	US-10-240-452-7	Sequence 7, Appli
44	50.2	4.1	6161	14	US-10-311-455-384	Sequence 384, App
45	50.2	4.1	6494	14	US-10-311-455-1366	Sequence 1366, Ap

ALIGNMENTS

RESULT 1

US-10-312-841-2
; Sequence 2, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (379615)
US-10-312-841-2

Query Match 4.9%; Score 59.8; DB 14; Length 3673778;

Best Local Similarity 46.3%; Pred. No. 0.24;

Matches 196; Conservative 0; Mismatches 227; Indels 0; Gaps 0;

Qy	797	TATAGTACAAAAAGTCATGAGCTTATTCGCTCATGACTTTTCGTTTAAAGATTTTTT	856
Db	1064838	TTTAGTGAATAGTAATGATATTATGATTAAATAATTAATTAATAAGTATT	1064897
Qy	857	AAATAAGTTAATCACTTTTATGAACCTATCTTATTAATTGATAGTACGTAAGTTTAC	916
Db	1064898	AATATTATTTATTTTATTTATATTTTATGAAAATAATAGTATAATGATTAGTTT	1064957
Qy	917	ATCATTAGGAGTATCTTGTGAGCAATCATCACTTCCTTACTGTGATGGTCAATCCCA	976
Db	1064958	TATGTAATTTGTTTGTGTTTATAGATTTTGTAGAAAGTTGTTTTTATGATATTATTAAGA	1065017

Qy	977	TATGAATAATTTTTTATAGTCCTCGAAGTAATCCACATATCACAGTCTATTAA	1036
Db	1065018	AATAAGTTTTPAGATTATAGAGTGATATTTPAATCGTAATPAATATATATATTGTGATTTA	1065077
Qy	1037	ATCTGATCCTCTTCATCTAATGTTAATTTTCCTTTTTGGCGGTATCCCATACTGTTAAAT	1096
Db	1065078	TTATAATTGCTATATGTTATTGAAATTTTAGTTAGTGAGTAAAATATTTTGT	1065137
Qy	1097	GAAATGTTTTAAATTCATCTGTTTGTGGAGAAGATATCCCTTTTGTGTTTAAATTGACTC	1156
Db	1065138	TATTTTTTTTTTATTTTGATTTTAAATTTATTTTATAATTAATATTTTTTGTGTTTAAAG	1065197
Qy	1157	GACATGTATATCTTTTATTTCTTGTTTTCTTAAAGACAGGGGGCTCATTTGGGTCTCT	1216
Db	1065198	TTTGATGTAATAGTTTATTTATTTTTTTTTTATATATAGTATTATTTTAAATTAATTTTGT	1065257
Qy	1217	TTG 1219	
Db	1065258	TTG 1065260	

RESULTS, T. 2

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US-10-424-599-57885
; Sequence 57885, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 57885
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(673)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_23282C.1
US-10-424-599-57885

```

	Query Match	4.7%	Score 57.8;	DB 12;	Length 673;
	Best Local Similarity	47.3%;	Pred. No. 0.0094;	Mismatches 173; Conservative	Gaps 0;
QY	819	TTAATTCGCTCATGACACTTTTTCGGTTAAATGATTTTTTTAAATAAGTATTAAACCTTTTGA	878		
Db	304	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTTTATTTGTTTATTTTTT	363		
QY	879	GAACATCTCTCAATTAAATTCATAGTAGCTAAGGTTTACATCATTAGGAGTATCTTGTTGA	938		
Db	364	TATATTTTTTAAATTTTTTTTTTTTATTTTTTTTATGTATTTTATGTTTTTTTTTTTTTT	423		
QY	939	GCAATCATCACTTCGTTACTGTGATGGTCAACTACCCATATGAATAATTTTTTAAAGTC	998		
Db	424	GTAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTTTTTTTTTTTT	483		
QY	999	CCATCCCGAAAGTAATCCACATATCACGCTATTTAAATCTGATCCTCTTCATCTAAT	1058		
Db	484	TTTTTTTTTTTATTTTATTTTTTTTNAATTTATTTTAGTTTTTTTTTTTTTATTTTTATTT	543		
QY	1059	GTTAAATTTTCCTTTTGGCGGTATCCATCTGTTAATGAATGTTTTTAAATCATCTGTT	1118		
Db	544	TTTATTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTTTTTTTTTTTTTGTTTTTTATTTTTT	603		
QY	1119	TTTGTGAAAAGATATCCTTTTTTGTTTTTTAATTGACCTCGACATGATATCTTTATTCT	1178		

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Db      604 TTTTATTTTTTTTTTTTTTTTTTTTTTTGTAATTTTTTTTTTTTTTTT 663
Qy      1179 TGTTTT 1184
          |||||
Db      664 TTTTTT 669

RESULT 3
US-10-312-841-1
; Sequence 1, Application US/103112841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerha
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

```

Query Match	4.6%;	Score 56;	DB 14;	Length 3673778;
Best Local Similarity	44.8%;	Pred. No. 1.6;		
Matches 215;	Conservative 0;	Mismatches 265;	Indels 0;	Gaps 0;
QY	663	TGGGGATTTCAGATTCAGAAATAGCTTTATCTTCAATTAACAGTTTAAAAAGAGCTGTGAT	722	
Db	2552436	TGGGATATTTTTTTTAAATTTATTTATTTGTTAAAGTTTGTGTGAATGTTTAAAGAGTT	2552495	
QY	723	GAAGAAGAACCCGATGTTTTCTTTGGACATGATATAGACAGAGAAAGGGATGTTAAAGT	782	
Db	2552496	TTAATAATAATTTTGTATTAGATTTTTTTCAGTTTATTAGTTATTGTTAGAGTTTTTGTTTT	2552555	
QY	783	GTTCCTCGAATATATATAGTACAAAAAGTCATGAGCTATTTCGCTCATGACTTTTTTCGTT	842	
Db	2552556	GGTAATATAATAGAAATATTGTAATGGTGTATAATTTTCAGTTATATTGGTTCGTTGTA	2552615	
QY	843	TAAATGATTTTTTTTAAATAAGTTTATAAACTTTTTTATAGAACTATCTCTCAATTAATGATAG	902	
Db	2552616	TTAGTCTGTTGTTTACGTCGGTTTTAAAAATTTTTTTTATTTTTTTTAAAAATTAATAAATG	2552675	
QY	903	TACGTAGGHTTTACATCAATTTAGGAGTATCTGTTTGAGCAATCATCACTTCGTTACTGTGA	962	
Db	2552676	TTAGAAATGGGTTT	2552735	
QY	963	TGGTCAACTACCCATATGAATAATTTTTTATAAGTCCCATCCGAAAGTAATCCACATA	1022	
Db	2552736	TTTTTTTTTGTTATT	2552795	
QY	1023	TCACAGTCTATTAATCTGATCCCTCTTCACTAAAGTTAAATTTCTCTTTTTTGGCGGTA	1082	
Db	2552796	TTTTTTTTTTTTTTTTTAAATT	2552855	
QY	1083	TCCATCTGTTAAATGAATGTTTTTAAATCTATCTGTTTTGTGAGAAAGATATCCTTTTTT	1142	
Db	2552956	TGTTTTTACGTTTTTTTTTTTATTTAGCTTTTGATATTTTTTATGTTTTCGTTATATTTTTT	2552915	

RESULT 4
US-10-311-455-240
; Sequence 240, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander


```
Query Match 4.5%; Score 54.8; DB 9; Length 516;
Best Local Similarity 46.0%; Pred. No. 0.038;
Matches 182; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

QY 793 TATATAGTACAAAAGTCATGAGCTTATTCGTCATGACTTTTCGTTAAAGATTT 852
DB 38 TGTATAGAGTTAAATCTTAAATGCAATAGGATATNGAGGTAGTTTATATTT 97

QY 853 TTTTAAATAAGTTATAAAGCTTTTAAAGACTATCTTCATTAATGATAGTAAAGT 912
DB 98 GTTTTGTATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 157

QY 913 TTATCAATTTAGAGATCTTGTGTGACATCACTTCGTTACTGTGATGTCACACTA 972
DB 158 TTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 217

QY 973 CCCATATGAATAATTTTTTATAAGTCCATCCCTCGAAAGTAATCCACATATCACAGTCTA 1032
DB 218 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 277

QY 1033 TTAATCTGATCCCTTCTTCACTAAAGTTAAATTTTCCTTTTGGCGGTATCCATCTGT 1092
DB 278 TATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 337

QY 1093 TAATGATGTTTAAATCACTCTGTTTTCTGTGAGAAAGATATCCTTTTGTGTTTAAATG 1152
DB 338 TAAATTTTGTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 397

QY 1153 ACTCGACATGTATATCTTTTATTTCTTGTGTTTCCCTA 1188
DB 398 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 433

RESULT 7
US-10-221-613-33
; Sequence 33, Application US/10221613
; Publication No. US20040029123A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
; FILE REFERENCE: 5013.1004
; CURRENT APPLICATION NUMBER: US/10/221.613
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/EP01/02945
; DE 10013847.00
; DE 10019058.8
; DE 10019173.8
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-03-15
; 2000-03-15
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 428
; SEQ ID NO 33
; LENGTH: 6109
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (214, 2796..2797, 4347)
US-10-221-613-33

Query Match 4.5%; Score 54.8; DB 12; Length 6109;
Best Local Similarity 47.2%; Pred. No. 0.13;
Matches 167; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

QY 835 TTTTCGTTAAATGATTTTTTAAATAAGTTATAAACTTTTTTGAAGACTATCTTCATTTA 894
DB 1741 TTTTATTAATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1800

QY 895 ATTGATAGTACGTAAGGTTTACATCATAGGAGTATCTTGTGAGCAATCATCATTCTGT 954
DB 1801 TTTTATTAATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1860

QY 955 TACTGTGATGCTCAACTACCCATATGAATATTTTATTAAGTCCCATCCCGAAAGTAA 1014
DB 1861 TTTTATTAATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1920

QY 1015 TCCACATATCACAGTCTATTAATCTGATCCTTCTTCAATCAATAATGTTAAATTTTCCCTTT 1074
DB 1921 TATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1980

QY 1075 TGCGGTATCCATPACTGTTAAATGAAATGTTTTTAAATTCATCTGTTTTTGAGAAAGATAT 1134
DB 1981 CGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 2040

QY 1135 CCTTTTGTGTTTAAATGACTCGACATGTATATCTTTTATTTCTGTTTTCCTA 1188
DB 2041 TATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 2094

RESULT 8
US-10-311-455-299
; Sequence 299, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Deter
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311.455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 299
; LENGTH: 6109
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: 214, 2796..2797, 4347
; OTHER INFORMATION: n is a or g or c or t
US-10-311-455-299

Query Match 4.5%; Score 54.8; DB 14; Length 6109;
Best Local Similarity 47.2%; Pred. No. 0.13;
Matches 167; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

QY 835 TTTTCGTTAAATGATTTTTTAAATAAGTTATAAACTTTTTTGAAGACTATCTTCATTTA 894
DB 1741 TTTTATTAATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1800

QY 895 ATTGATAGTACGTAAGGTTTACATCATAGGAGTATCTTGTGAGCAATCATCATTCTGT 954
DB 1801 TTTTATTAATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1860

QY 955 TACTGTGATGCTCAACTACCCATATGAATATTTTATTAAGTCCCATCCCGAAAGTAA 1014
DB 1861 TTTTATTAATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1920
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[illegible]

RESULT 9

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US-10-311-455-1497
; Sequence 1497, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Cytosine Methylation Level of a Specific Cytosine
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1497
; LENGTH: 6035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1497

```

Query Match	4.4%	Score 53.4	DB 14	Length 6035
Best Local Similarity	46.8%	Pred. No. 0.25		
Matches 168	Conservative 0	Mismatches 191	Indels 0	Gaps 0
QY	831	GAC	TTTTTCGTTAAATGATTTTTTTAAATAAGCTATATAAAGCTTTTATAGACATATCTTCA	890
DB	32	GATAGTTTGTTGAGATGAGGTTTTTAGTTTATTTATGTTTTTATAAAATTTATATGTA	91	
QY	891	TTTAAATGATGACGTAAAGGTTTACATCATAGGAGTATCTGTCGAGCAATCATCACT	950	
DB	92	TATATATTTTAGTGATATTTTGTTATTAAGTTTGATTAITTTTTTTTAGTTGAATTTTG	151	
QY	951	TCGTTACTGATGCTGCACTACCCATATAGAAATATTTTTTATAAGTCCCATCTCGAAA	1010	
DB	152	TGPTATTTTTTGTTTTTTGTTTTTAGGTATTTTATATTTGTTTTATGAATAAGGTTATTTT	211	
QY	1011	GTAATCCACATATCACAGTCTATTAATCTGATCCCTCTTCACTAATGTTAATTTTCCT	1070	
DB	212	TTTATTGTGATGTGT	271	
QY	1071	TTTTTGGCGGTATCCCATCTGTTAATGAATGTTTTTTAATTCATCTGTTTTTGTGAGAAAG	1130	
DB	272	ATTATGTTGTTATTATGAAGTGTATGTTTAAAGGAAAGTTTATTAATTAATTAAGATT	331	
QY	1131	ATATCCTTTTTTGTTTTTAATGTACTGCACATGATATCTTTTATATCTGTTTTCCTPAA	1189	
DB	332	TTATTTTTTATTTTTTGAAAGTGAATAATAATGTAAAAAATTTTTTAAAGTGTATTGTAA	390	

RESULT 10

US-10-311-455-2128
US-10-311-455-2128 ; Sequence 2128, Application US/10311455

```

; Publication No. US20030143606A1
;
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
;
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System b
;
; TITLE OF INVENTION: cytosine methylation
;
; FILE REFERENCE: 5013.1014
;
; CURRENT APPLICATION NUMBER: US/10/311,455
;
; CURRENT FILING DATE: 2002-12-16
;
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
;
; PRIOR FILING DATE: 2001-07-02
;
; PRIOR APPLICATION NUMBER: DE 10032529.7
;
; PRIOR FILING DATE: 2000-06-30
;
; PRIOR APPLICATION NUMBER: DE 10043826.1
;
; PRIOR FILING DATE: 2000-09-01
;
; NUMBER OF SEQ ID NOS: 2424
;
; SEQ ID NO 2128
;
; LENGTH: 15548
;
; TYPE: DNA
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;
; US-10-311-455-2128

```

Query Match	4.4%;	Score 53.4;	DB 14;	Length 15548;
Best Local Similarity	46.8%;	Pred. No. 0.41;		
Matches 168;	Conservative 0;	Mismatches 191;	Indels 0;	Gaps 0;
QY	834	TTTTTCGTTTAAATGATTTTTTTTTAAATAAGTTTATAAACTTTTTTTAGAACTATCTTCATTT	893	
Db	11655	TTTTTATATTTATTTTATTTTATATTTTATATTTTATTTTATTTTATTTTATTTATTTAT	11714	
QY	894	AAATGATAGTAGCTAAGGTTTACATCATTTAGGAGTATCTTGTCGAGCAATCATCACTTTCG	953	
Db	11715	TTTATTTTTTATATTTTATTTTATATTTATTTATTTATTTATTTTATTTTATTTTATTTT	11774	
QY	954	TTACTGTGATGCTCACTACCCATATGAAATATTTTTTTTATAAGTCGCCATCTCCGAAAGTA	1013	
Db	11775	TATATTTTATTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	11834	
QY	1014	ATCCACATATCACAGTCATTTAAATCTGATCCTTCCTTCATCTAATGTTAAATTTTCCTTTT	1073	
Db	11835	ATTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	11894	
QY	1074	TTGGCGGTATCCATACTGTTTAAATGAATCTTTTAAATTCATCTGTTTTTGTGAGAAAGATA	1133	
Db	11895	TATATTTATTTTATTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATA	11954	
QY	1134	TCCTTTTTTGGTTTTAAATGACTCGACATGATATATCTTTTATTTCTTGTTTTCCCTAAAAA	1192	
Db	11955	TGTTATATATATTTTATTTTATATGTTATATATATTTTATTTTATTTTATATGTTATATATA	12013	

RESULT 11

US-10-233-676-95
Sequence 95, Application US/10239676
Publication No. US20030082609A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
2000-04-06

; 2000-04-07		; TYPE: DNA	
; 2000-06-30		; ORGANISM: Artificial Sequence	
; 2000-09-01		; FEATURE:	
; NUMBER OF SEQ ID NOS: 228		; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)	
; SEQ ID NO 95		US-10-240-453-107	
; LENGTH: 15732		Query Match	
; TYPE: DNA		4.4%; Score 53.2; DB 14; Length 15732;	
; ORGANISM: Artificial Sequence		Best Local Similarity 47.5%; Pred. No. 0.45;	
; FEATURE:		Matches 189; Conservative 0; Mismatches 208; Indels 1; Gaps 1;	
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)			
US-10-239-676-95			
; 796 ATATAGTACAAAAGTCATGAGCTTATTCG-CTCATGACCTTTTTCGTTTAAATGATTTT 854		Qy	
; 6770 AGATAGTAAATAATTAATTAAGTATTTGTTGATTTTTCGTTTAAATGATTTT 6829		Db	
; 855 TTAATAAGTTATATAAATCTTTTATAGAACTATCTTCATTTAATGATAGTACGTAAGTTT 914		Qy	
; 6830 ATTTTTAGATTTATTTTTTATATAGTAGTCTTTTATATAAGAGTTGTGGGTATGG 6889		Db	
; 915 ACATCATGAGGATCTCTGTCGAGCAATCATCTTCGTTACTGTGATGGTCAACTACC 974		Qy	
; 6890 ATATTTTATGTTAGTTTTCGAAAGTTTGAATATAATAATTTTAAATTTT 6949		Db	
; 975 CATATGAATATATTTTTTATAGTCCCATCTCGAAAGTAAATCCACATATCACAGTCTATT 1034		Qy	
; 6950 GTTAAAGAAATATGTAATAATAAATGCTTATTTTAAATAGTTTAAAGTATAGTTT 7009		Db	
; 1035 AAATCTCATCTCTTCATCTAATGTTAAATTTTCCTTTTGGCGGTATCCATCTGTTA 1094		Qy	
; 7010 AGTAAATAATATATTTATATGTTGTGTAATTAATTTTAAAGAGTTTGTGATTTGTA 7069		Db	
; 1095 ATGAATGTTTAAATCTGTTTTCGTAAGAGATATCTTTTTCCTTAAATTTTAAATGAC 1154		Qy	
; 7130 TAAATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 7167		Db	
RESULT 12			
US-10-453-107		US-10-453-107	
; Sequence 107, Application US/10240453		; Sequence 654, Application US/10311455	
; Publication No. US2003014826A1		; Publication No. US2003014360A1	
; GENERAL INFORMATION:		; GENERAL INFORMATION:	
; APPLICANT: OLEK, Alexander		; APPLICANT: OLEK, Alexander	
; APPLICANT: PIERBROCK, Christian		; APPLICANT: PIERBROCK, Christian	
; APPLICANT: BERLIN, Kurt		; APPLICANT: BERLIN, Kurt	
; TITLE OF INVENTION: Transcription		; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting	
; TITLE OF INVENTION: By Means of Assessing the Methylation Status of Genes Associated with DNA		; TITLE OF INVENTION: cytosine methylation	
; TITLE OF INVENTION: With DNA Transcription		; FILE REFERENCE: 5013.1014	
; FILE REFERENCE: 5013.1009		; CURRENT APPLICATION NUMBER: US/10/311,455	
; CURRENT APPLICATION NUMBER: US/10/240,453		; CURRENT FILING DATE: 2002-12-16	
; CURRENT FILING DATE: 2002-10-02		; PRIOR APPLICATION NUMBER: PCT/EP01/07537	
; PRIOR APPLICATION NUMBER: PCT/EP01/03973		; PRIOR FILING DATE: 2001-07-02	
; PRIOR FILING DATE: 2001-04-06		; PRIOR APPLICATION NUMBER: DE 10032529.7	
; PRIOR FILING DATE: 2000-04-06		; PRIOR FILING DATE: 2000-06-30	
; PRIOR FILING DATE: 2000-04-07		; PRIOR APPLICATION NUMBER: DE 10043826.1	
; PRIOR FILING DATE: 2000-06-30		; PRIOR FILING DATE: 2000-09-01	
; PRIOR APPLICATION NUMBER: DE 10043826.1		; NUMBER OF SEQ ID NOS: 2424	
; NUMBER OF SEQ ID NOS: 350		; SEQ ID NO 654	
; LENGTH: 15732		; LENGTH: 6436	
		; TYPE: DNA	
		; ORGANISM: Artificial Sequence	
		; FEATURE:	
		; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)	
		US-10-311-455-654	
		Query Match	
		4.3%; Score 53; DB 14; Length 6436;	
		Best Local Similarity 45.8%; Pred. No. 0.32;	
		Matches 182; Conservative 0; Mismatches 215; Indels 0; Gaps 0;	
		Qy 793 TATATATAGTACAAAAGTCATGAGCTTATTCGCTCATGACTTTTCGTTTAAATGATTT 852	

Db 3000 TATTATTAATAATATTTTATATATTTTAAAGCGTTATGATTTTATAATTTATTA 3059
Qy 853 TTTTAAATAAGTTATAAATTTTTTTAGAACATATCTTCATTTAAATGATAGTACGTAAGGT 912
Db 3060 TTTTAAATTTATTAATAAGTTAGAAAAAATGATATATTAATGATTTGTAAGAAATAT 3119
Qy 913 TTACATCATAGGAGTATCTTTGTGAGCAATCATCTTCCTTACTGTGATGGTCAACTA 972
Db 3120 TTTAAATTTAGGGTTATGAAGAAAGGTATTTTGAATTAATGAATATAGTGGAAAAA 3179
Qy 973 CCCATATGAATAATTTTTTATAAGTCCCATCTCGAAAGTAATCCACATATCACAGTCTA 1032
Db 3180 TAAATATATATGATAAAATTTTGATAGTTGAGGATATGAATCAAAAATAAATTTT 3239
Qy 1033 TTAATCTGATCTCTCTTCATCTAATGTTAAATTTTCCCTTTTGGCGGTATCCATCTGT 1092
Db 3240 TTTGTTTTTTTTTTTAAAGTTGTTATTTGATTAATTAAGTTTTTTTTTTTTTTTTTTT 3299
Qy 1093 TAAATGAATGTTTTTAAATTCATCTGTTTTGTGAGAAAGATATCCTTTTGTGTTTAAATG 1152
Db 3300 TT 3359
Qy 1153 ACTCGACATGATATCTTTTATTTCTTGTGTTTCTCTAA 1189
Db 3360 TT 3396

RESULT 14
US-10-257-166-150
; Sequence 150, Application US/10257166
; Publication No. US20040023230A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
; TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
; FILE REFERENCE: 5013.1011
; CURRENT APPLICATION NUMBER: US/10/257,166
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/EP01/07470
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-06-29
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 150
; LENGTH: 8776
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-150

Query Match 4.3%; Score 53; DB 16; Length 8776;
Best Local Similarity 46.8%; Pred. No. 0.37;
Matches 167; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

Qy 832 ACTTTTTCGTTTAAATGATTTTTTTTAAATAAGTTATTAACCTTTTGAACATCTTCAT 891
Db 6852 AATAATTTTGGAAATTAATTTTTTAAATATATTTTAAATATTAATTTTGAATTTTGA 6911
Qy 892 TTAATTCATAGTACGTAAGGTTTATCATCATAGGAGTATCTTTGTGAGCAATCATCACT 951
Db 6912 ATATTTTTTGTGTTTGGTATAAAATGTAATTTAGGTTTATTTTGAATATTTTAAAT 6971
Qy 952 CGTTACTGTGATGGTCAACTACCAATGAAATATTTTTTATAAGTCCATCCCTCGAAG 1011
Db 6972 TGGTTTTTGAATTAGTTATTTTTTTTAAAGTGTGTTTTTTTTTTAGTGGAAAAATGG 7031
Qy 1012 TAAATCCACATATCAGTCTAATTAATCTGATCTCTTCACTAATGTTAATTTTCCCT 1071

Db 7032 TAATAAGTTAAGATTTGGTTATTAAGTGTGTTTATGTTATGTTAAAGTGTATTTT 7091
Qy 1072 TTTTGGCGGTATCCATATCTGTTTAATGAATGTTTTTAAATTCATCTGTTTTGTGAGAA 1131
Db 7092 AGTTTATTAGTGGAGAGAGTACGGAGTATATGTTTTTTTGTATATATATAATAATA 7151
Qy 1132 TATCCTTTTTTTGTTTTTAAATGACGTCGACATGATATCTTTTATTTCTTTGTTTCT 1188
Db 7152 TATATATATTTATGTTTATTTAAATATTTTGTGTTTTTTTGTATTTTATTTATTA 7208

RESULT 15
US-10-211-179-11/c
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTIGENSE MODULATION OF PHOSPHOTYROSYL PHOSPHATASE ACTIVATOR EXPRI
; FILE REFERENCE: PFS-0011
; CURRENT APPLICATION NUMBER: US/10/211,179
; CURRENT FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 119
; OTHER INFORMATION: n = a, t, c, or g
US-10-211-179-11

Query Match 4.3%; Score 52.8; DB 16; Length 158001;
Best Local Similarity 43.2%; Pred. No. 1.7;
Matches 252; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

Qy 608 TATTAAGGATTTGATGTCATCGTATACGAAAGAGAAATTTTGAAAAAGAGTGCATTTGG 667
Db 127542 TATTTATATATTTATATATTTTATATATATTTATATATTTATATATTTATATAT 127483
Qy 668 GATTTGATTCAGAAATAGCTTTATCTTCAATTAACCGTTTTAAAAAGAGTGTGTGAAG 727
Db 127482 TATTTTTTATATATATATATATTTTATATATTTTATATATATATATATATATAT 127423
Qy 728 AGAGCCGATGTTTCTTTGGACATGATATAGACGAGGAGGAGTGAAGTGTTCC 787
Db 127422 ATATTTATATATATATATATATATATATTTTATATATATATATATATATATATA 127363
Qy 788 CTGAATATATATAGTACAAAAAGTCATGAGCTTATTCGCTCATGACATTTTTCGTTTAAAT 847
Db 127362 TTTTATATATTTTATATATATATATATATATTTTATATATTTTATATATATATAT 127303
Qy 848 GATTTTTTAAATAAGTTATAAACTTTTTTAGAACTATCTTCAATTTAATTCATAGTAGCT 907
Db 127302 TATATATTTTATATATATATATATATATATATATATTTTATATATTTTATATATA 127243
Qy 908 AAGTTTACATCATTAGGAGTATCTTTGTTGAGCAATCATCATCTCGTTACTGTGATGGTC 967
Db 127242 ATATATTTATATATTTTATATATTTTATATAATAATATATATATTTTATATATATA 127183
Qy 968 AACTACCATATGAAATATTTTTTATAAGTCCCATCTCGAAAGTAATCCACATATCACA 1027
Db 127182 TATATATATATATATATATATTTTATATATTTTATATATATATATATATATATATA 127123
Qy 1028 GTCTATTAATCTGATCCCTTTCATCTAATGTTTAAATTTTCCCTTTTGGCGGTATCCAT 1087
Db 127122 TATTTATATATATATATATATATATATTTTATATATATTTTATATATTTTATATATA 127063
Qy 1088 ACTGTTAAATGAATGTTTTTAAATTCATCTGTTTTTGTGAGAAAGATATCCCTTTTGT 1147
Db 127062 TATTTATATATTTACAAATATATAAATATATTTATATATATATATATATATATATAT 127003
Qy 1148 AATTCAGTCCGACATGATATCTTTTATTTCTTTCTTTTCCCTAAA 1191
Db 127002 TTA 126959

Search completed: February 24, 2004, 05:42:50
Job time : 1456 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 01:02:27 ; Search time 415 Seconds
(without alignments)
12509.152 Million cell updates/sec

Title: US-10-019-661-1

Perfect score: 1222

Sequence: 1 cttactgtattgtttttatt.....tcatttgggtctctttgagt 1222

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_29Jan04.*

- 1: geneseqn1980s.*
- 2: geneseqn1980s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002s.*
- 7: geneseqn2003as.*
- 8: geneseqn2003bs.*
- 9: geneseqn2003cs.*
- 10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1222	100.0	1222	5	Aaf29642 Listeria
2	1037	84.9	1339	6	Abk47468 DNA encod
3	644.2	52.7	753	6	Abk47472 DNA encod
4	633.6	51.8	753	6	Abk47471 DNA encod
5	623.4	51.0	753	6	Abk47470 DNA encod
6	620.2	50.8	753	6	Abk47469 DNA encod
7	617	50.5	753	6	Abk47474 DNA encod
8	617	50.5	753	6	Abk47473 DNA encod
9	615.4	50.4	753	6	Abk47475 DNA encod
10	613.8	50.2	753	6	Abk47476 DNA encod
11	57	4.7	8056	7	Abz10246 Haematopo
12	56.6	4.6	7667	4	Aas46334 Tumour su
13	55.6	4.5	6419	6	Abi32267 Human imm
14	55.6	4.5	14006	6	Abi33958 Human imm
15	55.6	4.5	47108	6	Abk31511 Signal tr
16	54.8	4.5	516	7	Abx40620 Bovine ES
17	54.8	4.5	6109	6	Abi32326 Human imm
18	54.8	4.5	6109	6	Aas61077 Human gen
19	54.6	4.5	9742	6	Abi70479 Chemicall
20	54.6	4.5	11964	6	Abq67025 Human ang
21	54	4.4	975	6	Abq29508 Oligonuc
22	54	4.4	975	6	Abq29509 Oligonuc
23	53.8	4.4	61020	4	Aas46788 Tumour su

24	53.4	4.4	6035	6	ABL33524	Abi33524 Human imm
25	53.4	4.4	8056	7	ABZ10100	Abz10100 Haematopo
26	53.4	4.4	15548	6	ABL34155	Abi34155 Human imm
27	53.2	4.4	594	6	ABQ46990	Abq46990 Oligonuc
28	53.2	4.4	594	6	ABQ46991	Abq46991 Oligonuc
29	53.2	4.4	8056	7	ABZ10246	Abz10246 Haematopo
30	53.2	4.4	15732	4	AAS45388	Aas45388 Chemicall
31	53.2	4.4	15732	6	ABK28233	Abk28233 DNA trans
32	53	4.3	6436	6	ABL32681	Abi32681 Human imm
33	53	4.3	8776	6	ABK40068	Abk40068 Human che
34	52.6	4.3	9539	4	AAS45347	Aas45347 Chemicall
35	52.6	4.3	9539	6	ABK28180	Abk28180 DNA trans
36	52.6	4.3	11178	6	ABK31173	Abk31173 Signal tr
37	52.6	4.3	11178	6	ABL70508	Abi70508 Chemicall
38	52.6	4.3	11178	6	AAS61060	Aas61060 Human gen
39	52.4	4.3	446	7	ABX38235	Abx38235 Bovine ES
40	52.4	4.3	5032	6	AAS61083	Aas61083 Human gen
41	52.4	4.3	8079	6	ABL92313	Abi92313 Chemicall
42	52.2	4.3	6713	6	ABL33080	Abi33080 Human imm
43	52.2	4.3	6713	6	ABL34526	Abi34526 Human met
44	52.2	4.3	6713	6	ABL70251	Abi70251 Chemicall
45	52.2	4.3	7143	3	AAA70250	Aaa70250 Plasmodiu

ALIGNMENTS

RESULT 1

AAF29642	AAF29642 standard; DNA; 1222 BP.
XX	
AC	AAF29642;
XX	
DT	10-APR-2001 (first entry)
XX	
DE	Listeria sp. strain 240B1 aiiA gene.
XX	
KW	Listeria; aiiA; autoinducer inactivation protein A; antibacterial;
KW	disease resistance; soft rot disease resistance; bacterial infection; ds.
XX	
OS	Listeria sp.
XX	
PN	WO200102578-A1.
XX	
PD	11-JAN-2001.
XX	
PF	17-NOV-1999; 99WO-SG000128.
XX	
PR	02-JUL-1999; 99SG-00003146.
XX	
PA	(MOLE-) INST MOLECULAR AGROBIOLOGY 1 RES LINK.
XX	
PI	Lian-Hui Z, Yihu D, Jinling X;
XX	
DR	WPI; 2001-138146/14.
XX	
PT	New bacterial autoinducer inactivation proteins and nucleic acids
PT	encoding the protein, for increasing disease resistance, preventing or
PT	reducing bacterial damage to a plant or animal, or treating bacterial
PT	infections in animals.
XX	
PS	Claim 2; Fig 4A; 49pp; English.
XX	

The present sequence is a nucleic acid encoding a bacterial autoinducer inactivation protein (AiiA). It is useful for increasing disease resistance as well as preventing or reducing bacterial damage to a plant or animal. The nucleic acid may be used to confer resistance to diseases where expression of pathogenic genes are regulated by autoinducers, such as diseases caused by *Pseudomonas aeruginosa*, *Erwinia stewartii*, *Xenorhabdus nematophilus*, *Erwinia chrysanthemi*, *Pseudomonas solanacearum* and *Xanthomonas campestris*. It may also be used to confer soft rot disease resistance in susceptible plants such as potato, eggplant,

CC Chinese cabbage, carrot and celery. The bacterial autoinducer
CC inactivation protein may be directly used to treat or prevent bacterial
CC infections in animals including humans
XX
SQ Sequence 1222 BP; 376 A; 180 C; 238 G; 428 T; 0 U; 0 Other;

Query Match 100.0%; Score 1222; DB 5; Length 1222;
Best Local Similarity 100.0%; Pred. No. 5,8e-251;
Matches 1222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGTAATGTTTATTCAAACTAAAGTGAAGTGAATGATGACAGTAAG 60
Db |||||||
QY 1 CTTTACTGTAATGTTTATTCAAACTAAAGTGAAGTGAATGATGACAGTAAG 60
Db |||||||
QY 61 AAGCTTTATTTCCGTCAGCAGGTCGTTGATGTTGGATCATTCGTCGTTAATGATGAC 120
Db |||||||
QY 61 AAGCTTTATTTCCGTCAGCAGGTCGTTGATGTTGGATCATTCGTCGTTAATGATGAC 120
Db |||||||
QY 121 TTAACACGAGAGAAATTAATGAGTACCGGTTTGGTGTATCTTTTGGAGACTGAAGAA 180
Db |||||||
QY 121 TTAACACGAGAGAAATTAATGAGTACCGGTTTGGTGTATCTTTTGGAGACTGAAGAA 180
Db |||||||
QY 181 GGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAATGAAGTCTTTT 240
Db |||||||
QY 181 GGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAATGAAGTCTTTT 240
Db |||||||
QY 241 AACGGTACATTTGTCGAAGGCGAGGTTTACCGAAATGACTGAAGAGATAGATCGTG 300
Db |||||||
QY 241 AACGGTACATTTGTCGAAGGCGAGGTTTACCGAAATGACTGAAGAGATAGATCGTG 300
Db |||||||
QY 301 AATATTTTAAACGGGTTGTTATGAGCCGGAAGACCTCTTTATATATTAGTTCTCAC 360
Db |||||||
QY 301 AATATTTTAAACGGGTTGTTATGAGCCGGAAGACCTCTTTATATATTAGTTCTCAC 360
Db |||||||
QY 361 TTGCATTTTGCATATGACGAGGAAATGCGCTTTTATAATACCAATCATTTGTACAG 420
Db |||||||
QY 361 TTGCATTTTGCATATGACGAGGAAATGCGCTTTTATAATACCAATCATTTGTACAG 420
Db |||||||
QY 421 CGTGCTGAATATGAGCGGCGAGCATAGCGAAGATATTTGAAAGAAATGATATTCGCG 480
Db |||||||
QY 421 CGTGCTGAATATGAGCGGCGAGCATAGCGAAGATATTTGAAAGAAATGATATTCGCG 480
Db |||||||
QY 481 AATTTAACTACAAATCATTTGAGGTGATATGAGTCTGTCAGGAGTTCATTAATG 540
Db |||||||
QY 481 AATTTAACTACAAATCATTTGAGGTGATATGAGTCTGTCAGGAGTTCATTAATG 540
Db |||||||
QY 541 CATACACAGGCCATCTCCAGGCGCATCAATCGCTATTAAATGAGACAGAAATCCGGT 600
Db |||||||
QY 541 CATACACAGGCCATCTCCAGGCGCATCAATCGCTATTAAATGAGACAGAAATCCGGT 600
Db |||||||
QY 601 CCTGTAATTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db |||||||
QY 601 CCTGTAATTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db |||||||
QY 661 TTTGCGGGATTTGATTCAGANTTACGTTTATCTTCAATTAACGTTTAAAGAGAGTG 720
Db |||||||
QY 661 TTTGCGGGATTTGATTCAGANTTACGTTTATCTTCAATTAACGTTTAAAGAGAGTG 720
Db |||||||
QY 721 ATGAAGAGAGCCGATTTGTTTCTTTGGACATGATATGAGCAGGAAAGGGGATGATAA 780
Db |||||||
QY 721 ATGAAGAGAGCCGATTTGTTTCTTTGGACATGATATGAGCAGGAAAGGGGATGATAA 780
Db |||||||
QY 781 GTGTTCCCTGAT 840
Db |||||||
QY 781 GTGTTCCCTGAT 840
Db |||||||
QY 841 TTTAAATGATTTTTTAAATGAAGTTATAAATCTTTTGAAGTATCTTCAATTAATGAT 900
Db |||||||
QY 841 TTTAAATGATTTTTTAAATGAAGTTATAAATCTTTTGAAGTATCTTCAATTAATGAT 900
Db |||||||
QY 901 AGTACGTAAGGTTTACATCATTTAGGAGTATCTTGTGTAGCAATCATCTCGTACTGT 960
Db |||||||
QY 901 AGTACGTAAGGTTTACATCATTTAGGAGTATCTTGTGTAGCAATCATCTCGTACTGT 960
Db |||||||

QY 961 GATGTCACACTCCCATATGAAATATTTTTTATAAGTCCCATCTCGAAAGTAAATCCACA 1020
Db |||||||
QY 961 GATGTCACACTCCCATATGAAATATTTTTTATAAGTCCCATCTCGAAAGTAAATCCACA 1020
Db |||||||
QY 1021 TATCACAGTCTAATTAATCTGATCCTCTTTCATCTAATGTAATTTTCTTTTGGCGG 1080
Db |||||||
QY 1021 TATCACAGTCTAATTAATCTGATCCTCTTTCATCTAATGTAATTTTCTTTTGGCGG 1080
Db |||||||
QY 1081 TATCCATACGTTTAAATGAATGTTTAAATTCATCTGTTTGTGAGAAAGATATCCTTTT 1140
Db |||||||
QY 1081 TATCCATACGTTTAAATGAATGTTTAAATTCATCTGTTTGTGAGAAAGATATCCTTTT 1140
Db |||||||
QY 1141 TTGTTTAAATGACTCGACATGATATCTTTTATTTCTGTTTCTTAAAGACAGCGG 1200
Db |||||||
QY 1141 TTGTTTAAATGACTCGACATGATATCTTTTATTTCTGTTTCTTAAAGACAGCGG 1200
Db |||||||
QY 1201 GCTCAATTTGGTCTCTTTTGAGT 1222
Db |||||||
QY 1201 GCTCAATTTGGTCTCTTTTGAGT 1222
Db |||||||

RESULT 2
ABK47468
ID ABK47468 standard; DNA; 1339 BP.
XX
AC ABK47468;
XX
DT 29-AUG-2003 (revised)
DT 18-JUN-2002 (first entry)
XX
DE DNA encoding autoinducer inactivation protein AiiC.
XX
KW Autoinducer inactivation; AiiC; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; Erwinia carotovora; gene; ds.
XX
OS Bacillus thuringiensis; Cot1.
XX
FH Key Location/Qualifiers
FT CDS 166..918
FT /*tag= a
FT /product= "AiiC"
FT /note= "Autoinducer inactivation protein"
XX
FN WO200216623-A1.
XX
XX 28-FEB-2002.
XX
XX 23-AUG-2000; 2000WO-SG000123.
XX
XX 23-AUG-2000; 2000WO-SG000123.
XX
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX
XX Zhang L, Dong Y, Xu J, Zhang H;
XX
XX WPI; 2002-304123/34.
XX
XX P-PSDB; AAU78804.
XX
XX Polynucleotide encoding autoinducer inactivation protein, bacterium
XX having polynucleotide, and protein useful for increasing resistance to a
XX disease in sustainable plant or animal and for reducing bacterial damage.
XX
XX Claim 4; Fig 8; 82pp; English.
XX
XX The invention describes an isolated polynucleotide encoding an
XX autoinducer (N-acyl-homoserine lactone) inactivation protein. The
XX polynucleotide is useful for increasing disease resistance in a plant or
XX animal by introducing a polynucleotide into a cell of such a plant or
XX animal, in a manner that allows the cell to express the gene. The protein
XX is useful for reducing bacterial damage to a plant or animal preferably
XX human; and for reducing the formation of bacterial biofilms, by exposing

CC biofilm-forming bacteria to the autoinducer inactivation protein. A
 CC bacterial cell transformed with the polynucleotide, especially a plant or
 CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
 CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
 CC disease in a susceptible plant or animal, where virulence is regulated by
 CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
 CC This sequence encodes the autoinducer inactivation protein AiiC, the
 CC autoinducer inactivation activity of which is studied in the invention.
 CC (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 1339 BP; 425 A; 196 C; 251 G; 467 T; 0 U; 0 Other;

Query Match 84.9%; Score 1037; DB 6; Length 1339;
 Best Local Similarity 90.6%; Pred. No. 1.6e-211;
 Matches 1106; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 2 TTTACTGTATTGTTTATTCAAACTAAATGTAAGGTGGATACATATGACAGTAAAGA 61
 DB 119 TTTACTGTATTGTTTATTCCCAACTAAATGTAAGGTGGATACATATGACAGTAAAGA 178

QY 62 AGCTTTATTCGTCGCCAGCAGTGTGTATGTTGGATCATTCGTCTGTTAATAGTACAT 121
 DB 179 AGCTTTATTCGTTCCAGCAGTGTGTATGTTAGATCATCTTCTGTTAATAGTACAA 238

QY 122 TAACACGAGGAGAAATTATTAGACTTACCGGTTTGGTGTATCTTTTGGAGACTGAAGAAG 181
 DB 239 TCGGCGCGGGAATTTATTGAACTTACCTGTATGGTGTATCTTTTGGAGCGGAAGAAG 298

QY 182 GACCTATTTTATAGTACATACAGGTATGCCAGAAAGTGCAGTTTAATTAAGTCTTTT 241
 DB 299 GTCCCATTTTATAGTACATACAGGTATGCCAGAAAGTGCAGTTTAATTAAGTAAACTTTGTTG 358

QY 242 ACGGTACATTTTGTGCAAGGGCAGGTTTACGAAATGACTGAAGAGATGAATTCGTGA 301
 DB 359 AAGGGACATTTTGCAGAAAGGACAGAAATTTTACGAAATGACTGAAGAGATGAATTAATAG 418

QY 302 ATATTTTAAACGGGTGGTTATGAGCGGGAAGACCTTCTTTATATTATTAGTTCTCACT 361
 DB 419 CTATTTTAAACGGTGGAGGTATGAGCCAGATGACCTCTTATATTATTATTAGTTCACTT 478

QY 362 TGCATTTTGTATCATGCAAGGGAATGCGCTTTTATAAATPACCAATCATTTGTACAGC 421
 DB 479 TGCATTTTGTATCATGCAAGGGAATGCGCTTTTATAAATPACCAATCATTTGTACAGC 538

QY 422 GTGCTGAATATGAGCGCGCAGCATAGCGAAGAAATTTGAAAGAAATGTATATTCGCCGA 481
 DB 539 GTGCTGAATATGAGCGCGCAGCATATAGAGAGAAATTTTGAAGAGGTATATCTGCCGA 598

QY 482 ATTTAAACTACAAATCATTTGAAGGTGATATGAAGTCGTACAGGAGTTCAATTTATTCG 541
 DB 599 ATTTGAACACAAATTTATGAGGGGATATGAGTGTGTACAGGTTTCACTATTGT 658

QY 542 ATACACAGGCCATPACTCCAGGGCATCAATCGCTATTAAATTTGACACAGAAAAATCCGGTC 601
 DB 659 ATACACAGGACATTTACCGGGCATCAGTCACATATTAAATTTGACACAGAAAAATCTGGTG 718

QY 602 CTGTATTATTAAACGATTTGATCATCTGTATACGAAAGAGAAATTTGAAAAATGAAGTGCAT 661
 DB 719 TTGTGTTATTAAACCATTTGATGCATCTTATACGAAAGAGAAATTTTGAAGATGAAGTACCGT 778

QY 662 TTGCGGATTTGATTCAGAAATTTAGCTTTATCTTCAATTTAAACGTTTAAAGAAAGTGTGA 721
 DB 779 TTGCTGATTTGATCCAGAAATTTAGCTTTATCTTCAATTTAAACGTTTAAAGAAAGTGTGA 836

QY 722 TGAAGAGAGACCGGATTTGTTCTTTTGGACATGATATAGACGAGAAAGGGGATGTAAG 781
 DB 839 TGAAGAGAGACCGCTTGTGTTCTTTTGGACATGATATAGACGAGAAAGGGGATGTAAG 898

QY 782 TGTTCCTGAATATATATAGTACAAAAGCATGAGCTTATTCGCTCATGACTTTTTCGT 841
 DB 899 TGTTCCTGGAATATATATAGTACAAAAGCATGAGCTTATTCGCTCATGACTTTTTCGT 958

QY 842 TTAATGATTTTTTAAATAGTTATAAACTTTTTTAGAACTATCTTCATTTAATTTGATA 901

DB 959 TTAATGATTTTTTAAATAGTTATAAACTTTTTTGGAACTATCTTCATTTAATTTGATA 1018
 QY 902 GTACGTAAAGGTTTACATCATTTAGAGATCTTGTGTGCAATCATCACTTCGTTACTGTG 961
 DB 1019 GTACGTAAAGATTTACATCATTCAGAGATCTTGTGTGCAATCATCACTTCGTTACTATG 1078

QY 962 ATGCTCAACTACCATATGAAATATTTTATTAAGTCCCTCGAAAGTAATCCACAT 1021
 DB 1079 ATGATCAACTACCATATGAAATATTTTATAAGTACCATCTCTCAATGTAATCCACAT 1138

QY 1022 ATCACAGTCTATTAAATCTGATCTCTTCATCTAATGTTAATTTCTCTTTTGGCGGT 1081
 DB 1139 ATCAATCTATTAAATCTGATCTCTTCATCTAATGTTAATTTCTCTTTTGGCGGT 1198

QY 1082 ATCCATCTGTTAATGAATGTTTAAATTCATCTGTTTGTGAGAAAGATATCTTTT 1141
 DB 1199 ATTCATCTGTTAATGAATGTTTAAATTCATCTGTTTGTGAGAAAGATATCTTTT 1258

QY 1142 TGTTTAATGACTCGACATGATATCTTTTATTTCTTTTCTTAAAGACAGGGG 1201
 DB 1259 TGTTTAATGACTCGACATGATATCTTTTATTTCTGTTTCTCCAAAGACAGGGG 1318

QY 1202 CTCAATTTGGGTCTCTTTGAGT 1222
 DB 1319 CTCATTTGGATCCCTTTGAGT 1339

RESULT 3
 ABK47472
 ID ABK47472 standard; DNA; 753 BP.
 XX
 AC ABK47472;
 XX
 DT 29-AUG-2003 (revised)
 DT 18-JUN-2002 (first entry)
 XX
 DE DNA encoding autoinducer inactivation protein AiiG.
 KW Autoinducer inactivation; AiiG; N-acyl-homoserine lactone;
 KW disease resistance; bacterial damage reduction; biofilm;
 KW potato soft rot disease; *Erwinia carotovora*; gene; ds.
 XX
 OS *Bacillus thuringiensis*; B18.
 FH Key Location/Qualifiers
 CDS 1..753
 FT /*tag= a
 FT /product= "AiiG"
 FT /note= "Autoinducer inactivation protein"
 XX
 FN WO200216623-A1.
 XX
 XX 28-FEB-2002.
 XX
 XX 23-AUG-2000; 2000WO-SG000123.
 XX
 XX 23-AUG-2000; 2000WO-SG000123.
 XX
 PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
 XX
 PI Zhang L, Dong Y, Xu J, Zhang H;
 XX
 DR WPI; 2002-304123/34.
 DR P-PSDB; AAU78808.
 XX
 PT Polynucleotide encoding autoinducer inactivation protein, bacterium
 PT having polynucleotide, and protein useful for increasing resistance to a
 PT disease in sustainable plant or animal and for reducing bacterial damage.
 XX
 PS Claim 4; Fig 9; 82pp; English.
 XX
 CC The invention describes an isolated polynucleotide encoding an

CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably
CC human, and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This sequence encodes the autoinducer inactivation protein AiiF, the
CC autoinducer inactivation activity of which is studied in the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 753 BP; 243 A; 108 C; 172 G; 230 T; 0 U; 0 Other;

Query Match 52.7%; Score 644.2; DB 6; Length 753;
Best Local Similarity 91.0%; Pred. No. 7.8e-128;
Matches 685; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 49 ATGACAGTAAAGAGCTTTATTTTCGTCGCCAGCAGTCGTTGTATGTTGGATCATTCGCT 108
Db 1 ATGACAGTAAAGAGCTTTATTTTCGTCGCCAGCAGTCGTTGTATGTTGGATCATTCGCT 60
Qy 109 GTTAATAGTACATTAAACACGAGAGAAATATTAGACTTACCGGTTTGGTGTATCTTTG 169
Db 61 GTTAACAGTGGTTAAACCGGGGAAAACCTATTAAACTTTCGCGTTTGGTGTATCTTTG 120
Qy 169 GAGACTCAAGAGAGCCTATTATTAGTAGATACAGGTATGCCAGAAAGTGACAGTTAATAAT 228
Db 121 GAGACGGAAGAGGTCCTATTATTAGTAGACACAGGTATGCCAGAAAGTGACAGTTAATAAT 180
Qy 229 GAAGGCTCTTTTAAACGCTACATTTTTCGAGGGCAGGTTTTTACCGAAAATGACCTGAAGAA 288
Db 181 GAAGGCTCTTTTAAACGCTACATTTTTCGAAAGGACAGATTTTACCGAAAATGACCTGAAGAA 240
Qy 289 GATAGAAATCGTGAATATTAAACCGGTTGGTTATGACCGGAGAACCTTCCTTTATATT 348
Db 241 GATAGAAATCGTGAATATTAAACCGGTTGGTTATGACCGGAGAACCTTCCTTTATATT 300
Qy 349 ATTAGTTCTCACTTGCATTTTATCATGACGAGGAAATGCGCTTTTATATAATACACCA 408
Db 301 ATTAGTTGCGCACTTGCATTTTATCATGACGAGGAAATGCGCTTTTATATAATACGCA 360
Qy 409 ATCATTTGTACAGCGTGTGAATATGAGCGCGCAGCATATGCGGAAGAAATATTGAAAGAA 468
Db 361 ATCATTTGTACAGCGTGTGAATATGAGCGCGCAGCATATGCGGAAGAAATATTGAAAGAG 420
Qy 469 TGTATATTGCGGAATTTAACTACAAATCATTTGAAGGTGATTAAGTCGTACCAGGA 528
Db 421 TGCATATACACAGATTTAACTACAAATTTATGAAGGTGATTAAGTCGTACCAGGA 480
Qy 529 GTTCAATTTATGATACACAGGCACTACTCAGGGCATCAATCGCTATTAAATGAGACA 588
Db 481 GTTCCGTTATTGTATACACAGGCACTTCTCAGGGCATCAATCGCTATTAAATGAGACG 540
Qy 589 GAAAAATCCGGTCTGTATTATTAAACGATTCATCGATCGTATACGAAAGAGAAATTTGAA 648
Db 541 GAAAAATCCGGTCTGTATTATTAAACGATTCATCGATCGTATACGAAAGAGAAATTTGAA 600
Qy 649 AATGAAGTGCATTTGGGGATTTGATTCAGAAATAGCTTTATCTTCAATTAACGTTTA 708
Db 601 GATGAAGTACCGTTTGGCGGATTTGATTCGGAATTTAGCCTTTATCTTCAATTAACGTTTA 660
Qy 709 AAAGAAGTGGTGTATGAAGAGAGAGCCGATTCGTTTCTTGGACATGATATAGACAGGAA 768
Db 661 AAAGAAGTGGTGTATGAAGAGAGAGCCGATTCGTTTCTTGGACATGATATAGACAGGAA 720
Qy 769 AGGGGATGTAAGTGTTCCTCGAATATATATAG 801
Db 721 AAGGGATGTAAGTGTTCCTCGAATATATATAG 753

RESULT 4

ABK47471
ID ABK47471 standard; DNA; 753 BP.

XX ABK47471;

AC ABK47471;

XX 29-AUG-2003 (revised)

DT 18-JUN-2002 (first entry)

XX DNA encoding autoinducer inactivation protein AiiF.

XX Autoinducer inactivation; AiiF; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; *Erwinia carotovora*; gene; ds.

XX *Bacillus thuringiensis*; B17.

XX Key Location/Qualifiers

PH 1..753

FT /*tag= a

FT /product= "AiiF"

FT /note= "Autoinducer inactivation protein"

XX WO200216623-A1.

XX 28-FEB-2002.

XX 23-AUG-2000; 2000WO-SG000123.

XX 23-AUG-2000; 2000WO-SG000123.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX Zhang L, Dong Y, Xu J, Zhang H;

XX WPI: 2002-304123/34.

XX P-PSDB; AAU76807.

XX Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to a
PT disease in sustainable plant or animal and for reducing bacterial damage.

XX Claim 4; Fig 9; 82pp; English.

XX The invention describes an isolated polynucleotide encoding an
CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably
CC human, and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This sequence encodes the autoinducer inactivation protein AiiF, the
CC autoinducer inactivation activity of which is studied in the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 753 BP; 245 A; 105 C; 167 G; 236 T; 0 U; 0 Other;

Query Match 51.8%; Score 633.6; DB 6; Length 753;

Best Local Similarity 90.2%; Pred. No. 1.4e-125;

Matches 678; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 49 ATGACAGTAAAGAGCTTTATTTTCGTCGCCAGCAGTCGTTGTATGTTGGATCATTCGCT 108

Db 1 ATGACAGTAAAGAGCTTTATTTTCGTCGCCAGCAGTCGTTGTATGTTGGATCATTCCTCT 60

Db 421 TGTATATTACCGCATTTGAACTACAAAATATTGAGGGGATTATGAAGTGGTACCAGGT 480
Qy 529 GTTCAATATTGATACACACAGGCATACCTCCAGGGGATCAATCGCTATTAAATTGAGACA 588
Db 481 GTTCAATATTGATACACAGGCATACCTCCAGGGGATCAATCGCTATTAAATTGAGACG 540
Qy 589 GAAATATCCCGTCTGTATTATTAAACGATTGATCGCATCGTATACGAAAGAGAAATTTGAA 648
Db 541 GAGCAATCCCGTCTGTATTATTAAACGATTGATCGCATCGTATACGAAAGAGAAATTTGAA 600
Qy 649 AATGAAGTGGCATTTGCGGATTTGATTTCAGAAATAGCTTTATCTTCAATTAACAGTTTA 708
Db 601 GATGAAGTGGCATTTGCGGATTTGATTTCAGAAATAGCTTTATCTTCAATTAACAGTTTA 660
Qy 709 AAGAAGTGGTGTGAAAGAGAGCCGATTTGTTTCTTTGGAATGATATAGACAGGAA 768
Db 661 AAGAAGTGGTGTGAAAGAGAGCCGATTTGTTTCTTTGGAATGATATAGACAGGAA 720
Qy 769 AGGGGATGTAAGTGTTCCTCGAATATATATAG 801
Db 721 AAGAGTGTGATAGTGTTCCTCGAATATATATAG 753

RESULT 6

ID ABK47469 standard; DNA; 753 BP.

XX AC ABK47469;

XX XX 29-AUG-2003 (revised)
DT DT 18-JUN-2002 (first entry)

XX DNA encoding autoinducer inactivation protein AiiD.

XX Autoinducer inactivation; AiiD; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; Erwinia carotovora; gene; ds.
XX Bacillus thuringiensis; B1.

Key Location/Qualifiers
FH 1. 753
FT CDS /*tag= a
FT /product= "AiiD"
FT /note= "Autoinducer inactivation protein"

XX WO200216623-A1.

XX 28-FEB-2002.

XX 23-AUG-2000; 2000WO-SG000123.

XX 23-AUG-2000; 2000WO-SG000123.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX Zhang L, Dong Y, Xu J, Zhang H;

XX WPI; 2002-304123/34.

XX P-PSDB; AAU78805.

PT Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to a
PT disease in sustainable plant or animal and for reducing bacterial damage.

XX Claim 4; Fig 9; 82pp; English.

CC The invention describes an isolated polynucleotide encoding an
CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably

CC human; and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably *Bacillus thuringiensis*, which is from B1, B2,
CC B17, B18, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This sequence encodes the autoinducer inactivation protein AiiD, the
CC autoinducer inactivation activity of which is studied in the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 753 BP; 242 A; 113 C; 174 G; 224 T; 0 U; 0 Other;

Query Match 50.8%; Score 620.2; DB 6; Length 753;
Best Local Similarity 89.0%; Pred. No. 1e-122;
Matches 670; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 49 ATGACAGTAAGAAGCTTTATTTTCGTCGCCAGCGGTCTGTGTATGTTGGATCATCGTCT 108
Db 1 ATGACAGTAAGAAGCTTTATTTTCATCCAGCAGGTGCTTCATGTTGGATCATCGTCT 60
Qy 109 GTTAATAGTACATTAAACACGAGGAGATTATAGACTTACCGGTTTCGTTGTTATCTTTG 168
Db 61 GTTAACAGTGTGTTAACACCGGGGAACTATTAAACTTGCCTGCTGTGTTATCTTTT 120
Qy 169 GAGACTGAAGAAGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTGCAGTTTAATAAT 228
Db 121 GAGACGGAAGAAGGTCTCTATTTTAGTAGACACAGGTATGCCAGAAAGTGCAGTTTAATAAT 180
Qy 229 GAAGGTCTTTTAAACGGTACATTTCGAAGGGCAGGTTTTTACCGAAATGACTGAAGAA 288
Db 181 GAAGGTCTTTTAAACGGTACATTTCGTTGAAGGACAGATCTTACCGAAATGACTGAAGAA 240
Qy 289 GATGAATCGTGAATATTTTAAACGGTGTGTTATGACGGGAGACCTCTTTATATT 348
Db 241 GATGAATCGTGAATATATTAAAGCGTGTGGGGTATGACGGGACGACCTTTTATATT 300
Qy 349 ATTAGTTCTCACTTGTCAATTTTGATCATGCAGGAGGAAATGGCGCTTTTATAAATACACCA 408
Db 301 ATTAGTTCTCACTTGTCAATTTTGATCATGCAGGAGGAAACGGTCTTTTACAANTACACCA 360
Qy 409 ATCAATGTACAGCGTGTGTAATATGAGCGGGCGCAGCATAGCGGAAGAAATATTGAAAGAA 468
Db 361 ATTATTGTGACGCAACCGAATATGAGCGACACTTCATAGAGAAGAAATATATGAAAGAA 420
Qy 469 TGTATATTGCGGAATTTAAACTCAAAATCAATTCAGGTGATTATGAGTCGTACCGACGA 528
Db 421 TGTATATTACCGCATTTGAACTACAAAATTTATTGAAGGGGATTTGAGTGGTACCAGGT 480
Qy 529 GTTCAATTTATTGTCATACACAGGCATACCTCCAGGGCATCAATCGCTATTAAATTGAGACA 588
Db 481 GTTCAATTTATTGTCATACACAGGCATACCTCCAGGGCATCAATCGCTATTAAATTGAGACG 540
Qy 589 GAAAAATCCCGTCTGTATTATTAAACGATTGATCGCATCGTATACGAAAGAGAAATTTGAA 648
Db 541 GAGCAATCCCGTCTGTATTATTAAACGATTGATCGCATCGTATACGAAAGAGAAATTTGAA 600
Qy 649 AATGAAGTGGCATTTGCGGATTTGATTTCAGAAATAGCTTTATCTTCAATTAACAGTTTA 708
Db 601 GATGAAGTGGCATTTGCGGATTTGATTTCAGAAATAGCTTTATCTTCAATTAACAGTTTA 660
Qy 709 AAGAAGTGGTGTGAAAGAGAGCCGATTTGTTTCTTTGGAATGATATAGACAGGAA 768
Db 661 AAGAAGTGGTGTGAAAGAGAGCCGATTTGTTTCTTTGGAATGATATAGACAGGAA 720
Qy 769 AGGGGATGTAAGTGTTCCTCGAATATATATAG 801
Db 721 AAGAGTGTGATAGTGTTCCTCGAATATATATAG 753

RESULT 7

ID ABK47474 standard; DNA; 753 BP.

XX AC
XX ABK47474;
XX
XX DT 29-AUG-2003 (revised)
XX DT 18-JUN-2002 (first entry)
XX
XX DE DNA encoding autoinducer inactivation protein AiiI.
XX
XX KW Autoinducer inactivation; AiiI; N-acyl-homoserine lactone;
XX KW disease resistance; bacterial damage reduction; biofilm;
XX KW potato soft rot disease; Erwinia carotovora; gene; ds.
XX
XX OS Bacillus thuringiensis; B21.
XX
XX EH Key Location/Qualifiers
XX FT 1..753
XX FT /*tag= a
XX FT /product= "AiiI"
XX FT /note= "Autoinducer inactivation protein"
XX
XX PN WO200216623-A1.
XX
XX PD 28-FEB-2002.
XX
XX PF 23-AUG-2000; 2000WO-SG000123.
XX PR 23-AUG-2000; 2000WO-SG000123.
XX PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX PI Zhang L, Dong Y, Xu J, Zhang H;
XX
XX DR WPI; 2002-304123/34.
XX DR P-PSDB; AAU78810.
XX
XX PT Polynucleotide encoding autoinducer inactivation protein, bacterium
XX PT having polynucleotide, and protein useful for increasing resistance to a
XX PT disease in sustainable plant or animal and for reducing bacterial damage.
XX
XX PS Claim 4; Fig 9; 82pp; English.
XX
XX CC The invention describes an isolated polynucleotide encoding an
XX CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
XX CC polynucleotide is useful for increasing disease resistance in a plant or
XX CC animal by introducing a polynucleotide into a cell of such a plant or
XX CC animal, in a manner that allows the cell to express the gene. The protein
XX CC is useful for reducing bacterial damage to a plant or animal preferably
XX CC human; and for reducing the formation of bacterial biofilms, by exposing
XX CC biofilm-forming bacteria to the autoinducer inactivation protein. A
XX CC bacterial cell transformed with the polynucleotide, especially a plant or
XX CC animal bacterium preferably Bacillus thuringiensis, which is from B1, B2,
XX CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
XX CC disease in a susceptible plant or animal, where virulence is regulated by
XX CC autoinducers e.g. potato soft rot disease caused by Erwinia carotovora.
XX CC This sequence encodes the autoinducer inactivation protein AiiI, the
XX CC autoinducer inactivation activity of which is studied in the invention.
XX CC (Updated on 29-AUG-2003 to standardise OS field)
XX
XX SQ Sequence 753 BP; 233 A; 111 C; 177 G; 232 T; 0 U; 0 Other;

Query Match 50.5%; Score 617; DB 6; Length 753;
Best Local Similarity 88.7%; Pred. No. 4.9e-122;
Matches 668; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 49 ATGACAGTAAGAAGCTTTATTCGTCGCCAGAGTGTGTATGTTGGATCATTCGCT 108
Db 1 ATGACAGTAAGAAGCTTTATTCGTCGCCAGAGTGTGTATGTTAGATCATTCCTCT 60
Qy 109 GTTAATAGTACATTAAACACCGAGGAATTAATAGACTACCGGTTGGTGTATCTTTG 168
Db 61 GTTAATAGTACACTCGCGCCGGGAATTTATGAACCTACCTGATGCTGTATCTTTTG 120
Qy 169 GAGACTGAAGAAGACCTTTTATGATAGATACAGTATGCCAGAAAGTGCAATTAAT 228

Db 121 GAGACAGAAAGGGGCCCTATTTTAGATAGATACAGGTATGCCAGAAAGTGCGAGTTAATAAT 180
Qy 229 GAAGGTCTTTTAAACGGTACATTTGTTCGAAGGGCAGGTTTACCGAAAATGACTCAAGAA 288
Db 181 GAAGGGCTTTTAAACGGTACATTTGTTCGAAGGACAGATTTTACCGAAAATGACTCAAGAA 240
Qy 289 GATAGAAATCGTAATATTTTAAACGGTTCGGTTATGAGCCGGAGAGACTTCTTTTATATT 348
Db 241 GATAGAAATCGTAATATTTTAAACGGTTCGGTTATGAGCCGGAGAGACTTCTTTTATATT 300
Qy 349 ATTAGTCTCTCACTTTCATTCATCGACAGGAAATGCGCTTTTATAAATACACCA 408
Db 301 ATTAGTCTCTCACTTTCATTCATCGACAGGAAACGGTCTTTTACAATAACACCG 360
Qy 409 ATCATTTGACAGCGTGTGTAATATGAGCGCGGAGCATAGCAGAAATATTTGAAAGAA 468
Db 361 ATTATTTGACAGCGGCGGAATATGAGCGACACTTCATAGAGAGAAATATATGAAAGAA 420
Qy 469 TGTATATTGCGGAATTTAAACTACAAATCATTTGAAGGTGATTAAGTCTGTACCGAGA 528
Db 421 TGTATATTACCGCATTTGAACCTACAAAATTTATGAAGGGATTTAAGTGTGTCACGGT 480
Qy 529 GTTCAATTTATGTCATACACAGCGCATCTCCAGGGCATCAATCGCTATTATTAATGAGACA 588
Db 481 GTTCAATTTATGTCATACCGCGAGTCATCTCCAGGCCATCAGTCTGTATTCAITGAGACG 540
Qy 589 GAAAAATCCGGTCTCTGTATTATTAAACGATTGATGCATCGTATACGAAGAGAAATTTTCAA 648
Db 541 GACAAATCCGGTTCAGTTTATTAACTAATTTGATGATCGTACACGAAAGAGAAATTTTCAA 600
Qy 649 AATGAAGTGCCATTTGCGGGATTTGATTCAGAAATAGCTTTATCTTCAATTAACGTTTA 708
Db 601 GATGAAGTGCGGTTTCGCGAGGATTTGATCCAGAAATAGCTTTATCTTCAATCAAAAGTTTA 660
Qy 709 AAAGAAGTGTGTGAAGAAGAGAGCCGATTTGTTTCTTTCGACATGATATAGACGAGAA 768
Db 661 AAAGAAGTGTGGCGGAAGAGAAACCAATTTGTTTCTTGTGTCAATATATAGACGAGAA 720
Qy 769 AGGGAGTATAAGTGTTCCTCTGAATATATATAG 801
Db 721 AAGGGTTGTAGAGTGTTCCTCTGAGTATATATAG 753

RESULT 8
ABK47473
ID ABK47473 standard; DNA; 753 BP.
XX AC ABK47473;
XX
XX DT 29-AUG-2003 (revised)
XX DT 18-JUN-2002 (first entry)
XX
XX DE DNA encoding autoinducer inactivation protein AiiI.
XX
XX KW Autoinducer inactivation; AiiI; N-acyl-homoserine lactone;
XX KW disease resistance; bacterial damage reduction; biofilm;
XX KW potato soft rot disease; Erwinia carotovora; gene; ds.
XX
XX OS Bacillus thuringiensis; B20.
XX
XX EH Key Location/Qualifiers
XX FT 1..753
XX FT /*tag= a
XX FT /product= "AiiI"
XX FT /note= "Autoinducer inactivation protein"
XX
XX PN WO200216623-A1.
XX
XX PD 28-FEB-2002.
XX
XX PF 23-AUG-2000; 2000WO-SG000123.
XX

PR 23-AUG-2000; 2000WO-SG000123.
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
PA Zhang L, Dong Y, Xu J, Zhang H;
PI WPI; 2002-304123/34.
XX P-PSDB; AAU78809.
XX Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to a
PT disease in sustainable plant or animal and for reducing bacterial damage.
XX Claim 4; Fig 9; 82pp; English.
XX The invention describes an isolated polynucleotide encoding an
CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably
CC human; and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably Bacillus thuringiensis, which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by Erwinia carotovora.
CC This sequence encodes the autoinducer inactivation protein AiiJ, the
CC autoinducer inactivation activity of which is studied in the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
XX
SQ Sequence 753 BP; 235 A; 111 C; 176 G; 231 T; 0 U; 0 Other;

Query Match 50.5%; Score 617; DB 6; Length 753;
Best Local Similarity 88.7%; Pred. No. 4.9e-122;
Matches 668; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 49 ATGACAGTAAAGAGCTTTATTCCTCCAGCAGGTCTGTATGTTGGATCATTCGTCT 108
Db 1 ATGACAGTAAAGAGCTTTATTCCTCCAGCAGGTCTGTATGTTGGATCATTCGTCT 60

Qy 109 GTTAAATAGTACATTAACACGAGGAATTTATGACTTACCGTTTCGTGTATCTTTTG 168
Db 61 GTTAAATAGTACATTCGCGCGCGGGAATTTATGAACTTACCTGTATGTTATCTTTG 120

Qy 169 GAGACTGAAGAGGACCTATTTTAGTAGATACAGTATGCCAGAAAGTCAGTTAATAAT 228
Db 121 GAGACAGAGNAGGGCTATTTTAGTAGATACAGTATGCCAGAAAGTCAGTTAATAAT 180

Qy 229 GAAGGTCTTTTAAACGGTACATTTGTGGAAGGGCAGGTTTACCGAAATGACTGAAGAA 288
Db 181 GAAGGGCTTTTAAACGGTACATTTGTGGAAGGACAGATTTTACCGAAATGACTGAAGAA 240

Qy 289 GATAGATCGTGAATTTTAAACGGTTCGTTATGAGCGGAGACCTCTTTATATT 348
Db 241 GATAGATCGTGAATTTTAAACGGTTCGTTATGAGCGGAGACCTCTTTATATT 300

Qy 349 ATTAGTCTCTACTTTCATCTTTGATCATGACGAGGAAATGGCGCTTTTATAATACACCA 408
Db 301 ATTAGTCTCTACTTTCATCTTTGATCATGACGAGGAAACGGTCTTTTACAAATACACCG 360

Qy 409 ATCATTTGACGCTGTGAATATGAGCGCGGCGAGCATAGCGAAGATATTGAAAGAA 468
Db 361 ATTATTTGACGCGAGCGGAATATGAGCGAGCACTTCTATAGAGAGAAATATGAAAGAA 420

Qy 469 TGTATTTGCGCAATTTAACTACAAATCATTTGAAGGTGATTGAAGTCTGACAGGA 528
Db 421 TGTATTTACCGCATTTGAACTACAAATCATTTGAAGGGGATTGAAGTGTGACAGGT 480

Qy 529 GTTCAATTTATGATACACCGCGCATCTCCAGGGCATCAATCGCTATTAATGAGACA 588
Db 481 GTTCAATTTATGATACCGCGCATCTCTCCAGGCCATCAGTCGTCTTATTCATTGAGACG 540

Qy 589 GAAAAATCCGTCCTCTATTTAATTAACGATTGATGTCATCGTATACGAAAGAGAAATTTTGA 648
Db 541 GAGCAATCCGTTTCAGTTTTTATTAAACAATTTGATGTCATCGTACAGAAAGAGAAATTTTGA 600

Qy 649 AATGAAGTGCCATTTTCGGGATTTGATTCCAGAAATTAAGCTTTTATCTTCAATTAACCGTTTA 708
Db 601 GATGAAGTGCCGTTTCGAGGATTTGATCCAGAAATTAAGCTTTTATCTTCAATCAACGTTTA 660

Qy 709 AAAGAAAGTGCGTGAAGAAAGAGAGCCGATTTGTTTCTTTCGACATGATATAGACAGGAA 768
Db 661 AAAGGAGTGTGCGGGAAGAGAAACCAATTTGTTTCTTTCGTCATGATATAGACAGGAA 720

Qy 769 AGCGGATGTAAAGCTGTTCCCTGAATATATATAG 801
Db 721 AAGCGTTGTAGAGTGTTCCTGAGTATATATAG 753

RESULT 9
ABK47475
ID ABK47475 standard; DNA; 753 BP.
XX
AC ABK47475;
XX
DT 29-AUG-2003 (revised)
DT 18-JUN-2002 (first entry)
XX
DE DNA encoding autoinducer inactivation protein AiiJ.
XX
KW Autoinducer inactivation; AiiJ; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; Erwinia carotovora; gene; ds.
XX
OS Bacillus thuringiensis; B22.
XX
FH Key Location/Qualifiers
FT 1..753
FT /*tag= a
FT /product= "AiiJ"
XX /note= "Autoinducer inactivation protein"
XX
XX WO200216623-A1.
XX
XX 28-FEB-2002.
XX
XX 23-AUG-2000; 2000WO-SG000123.
XX
XX 23-AUG-2000; 2000WO-SG000123.
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX
XX Zhang L, Dong Y, Xu J, Zhang H;
XX
XX WPI; 2002-304123/34.
XX P-PSDB; AAU78811.
XX
XX Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to a
PT disease in sustainable plant or animal and for reducing bacterial damage.
XX
XX Claim 4; Fig 9; 82pp; English.
XX
XX The invention describes an isolated polynucleotide encoding an
CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably
CC human; and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably Bacillus thuringiensis, which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a

CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC this sequence encodes the autoinducer inactivation protein AiiK, the
CC autoinducer inactivation activity of which is studied in the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 753 BP; 234 A; 111 C; 177 G; 231 T; 0 U; 0 Other;

Query Match 50.4%; Score 615.4; DB 6; Length 753;
Best Local Similarity 88.6%; Pred. No. 1.1e-121;
Matches 667; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY	49	ATGACAGTAAAGAGCTTTATTTTCGTCGCCAGCAGGTCGTTGTATGTTGGATCATTCGTC	108
Db	1	ATGACAGTAAAGAGCTTTATTTTCATCCCGAGGTCGTTGTATGTTAGATCATTCCTCT	60
QY	109	GTTAATAGTACATTAACACAGGAGATTTATAGACTTACCGGTTTGGTGTATCTTTTG	168
Db	61	GTTAATAGTACACTCGCGCGGGGAATTTATGAACCTTACCTGTATGTTGTATCTTTG	120
QY	169	GAGACTGAAGAAGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAAT	228
Db	121	GAGACAGAAGAGGGGCTATTTTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAAT	180
QY	229	GAAGGTCCTTTTAAACGCTACATTTGTCGAAGGCGAGGTTTACCAGAAATGACTGAAGAA	288
Db	181	GAAGGGCTTTTAAACGCTACATTTGTTGAAGGACAGATTTTACCAGAAATGACTGAAGAA	240
QY	289	GATAGAAATCGTGAATATTTTAAACGGGTTGGTTATGAGCGGGAAGACCTTCTTTATAT	348
Db	241	GATAGAAATCGTGAATATTTAAAGCGGTAGGTTATGAGCGGGAAGACCTTCTTTATAT	300
QY	349	ATTAGTCTCATTGCATTTTGTATCATGACAGGAGGAAATCGCGCTTTTATAATACACCA	408
Db	301	ATTAGTCTCATTGCATTTTGTATCATGACAGGAGGAAATCGCGCTTTTATAATACACCG	360
QY	409	ATCATTTGTACAGCGTCTGTAATATGAGCGGCGCAGCATAGCGAAGATATTTGAAGAA	468
Db	361	ATTATTTGTGAGCGAGCGGGAATATGAGCGACACTTCTATAGAGAAGATATATGAAGAA	420
QY	469	TGTATATTGCGGAATTTAAACTAAATCATTTGAAGGTCATTTGAAGTCGTACACAGGA	528
Db	421	TGTATATTACCGCATTTGAACACTAAATTTATGAAGGGAATTTAGAGTGGTACACAGT	480
QY	529	GTTCAATATTGCAATACACAGCGCATCTCCAGGCGATCAATCGCTATTAATGAGACA	588
Db	481	GTTCAATATTGATAGCGCAGGTCATTTCTCCAGGCGCATCAGTCGTTATTTCAATTGAGACG	540
QY	589	GAAAAATCCGGTCTGTTATTTAAACGATGATGTCATCGTATACGAAGAGATTTTGA	648
Db	541	GAGCAATCCGGTTCAGTTTATTTAAACATTTGATGCAATCGTATACGAAGAGATTTTGA	600
QY	649	AATGAAGTGCCATTTGCGGGAATTTGATTTCAAGATTTAGCTTTATCTTCAATTAACGTTTA	708
Db	601	GATGAAGTGCCGTTGCGCAGGATTTGATCCAGAAATTTAGCTTTATCTTCAATCAACGTTTA	660
QY	709	AAGAAGTGTGATGAAGAAGAGCGGATTTTCTTGGACATGATATAGAGCAGGAA	768
Db	661	AAAGGAGTTGTGCGGGAAGAGAACCAATTTGTTTCTTGTGATATATAGAGCAGGAA	720
QY	769	AGGGGATGTAAGTGTTCCTCGAATATATATAG	801
Db	721	AAGGGTTGATAGAGTGTTCCTCGAATATATATAG	753

RESULT 10
ID ABK47476
XX ABK47476 standard; DNA; 753 BP.
AC ABK47476;
XX
DT 29-AUG-2003 (revised)
DT 18-JUN-2002 (first entry)

XX
DE
XX
XX
KW
KW
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OS
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FH
FT
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FT
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PN
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PD
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PF
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PR
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PA
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PI
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DR
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PS
XX
CC
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SQ
DNA encoding autoinducer inactivation protein AiiK.
Autoinducer inactivation; AiiK; N-acyl-homoserine lactone;
disease resistance; bacterial damage reduction; biofilm;
potato soft rot disease; *Erwinia carotovora*; gene; ds.
Bacillus thuringiensis; B25.
Key Location/Qualifiers
CDS 1..753
/*tag= a
/product= "AiiK"
/note= "Autoinducer inactivation protein"
MO200216623-A1.
28-FEB-2002.
23-AUG-2000; 2000WO-SG000123.
23-AUG-2000; 2000WO-SG000123.
(MOLE-) INST MOLECULAR AGROBIOLOGY.
Zhang L, Dong Y, Xu J, Zhang H;
WPI; 2002-304123/34.
P-PSDB; AAU78812.
Polynucleotide encoding autoinducer inactivation protein, bacterium
having polynucleotide, and protein useful for increasing resistance to a
disease in sustainable plant or animal and for reducing bacterial damage.
Claim 4; Fig 9; 82pp; English.
The invention describes an isolated polynucleotide encoding an
autoinducer (N-acyl-homoserine lactone) inactivation protein. The
polynucleotide is useful for increasing disease resistance in a plant or
animal by introducing a polynucleotide into a cell of such a plant or
animal, in a manner that allows the cell to express the gene. The protein
is useful for reducing bacterial damage to a plant or animal preferably
human; and for reducing the formation of bacterial biofilms, by exposing
biofilm-forming bacteria to the autoinducer inactivation protein. A
bacterial cell transformed with the polynucleotide, especially a plant or
animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
disease in a susceptible plant or animal, where virulence is regulated by
autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
this sequence encodes the autoinducer inactivation protein AiiK, the
autoinducer inactivation activity of which is studied in the invention.
(Updated on 29-AUG-2003 to standardise OS field)

Query Match 50.2%; Score 613.8; DB 6; Length 753;
Best Local Similarity 88.4%; Pred. No. 2.4e-121;
Matches 666; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY	49	ATGACAGTAAAGAGCTTTATTTTCGTCGCCAGCAGGTCGTTGTATGTTGGATCATTCGTC	108
Db	1	ATGACAGTAAAGAGCTTTATTTTCATCCCGAGGTCGTTGTATGTTAGATCATTCCTCT	60
QY	109	GTTAATAGTACATTAACACAGGAGATTTATAGACTTACCGGTTTGGTGTATCTTTTG	168
Db	61	GTTAATAGTACACTCGCGCGGGGAATTTATGAACCTTACCTGTATGTTGTATCTTTG	120
QY	169	GAGACTGAAGAAGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAAT	228
Db	121	GAGACAGAAGAGGGGCCATTTTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAAT	180
QY	229	GAAGGTCCTTTTAAACGCTACATTTGTCGAAGGCGAGGTTTACCAGAAATGACTGAAGAA	288

Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP; cytosine methylation; ds.

Homo sapiens.

WO200168912-A2.

20-SEP-2001.

15-MAR-2001; 2001WO-EP002955.

15-MAR-2000; 2000DE-01013847.

06-APR-2000; 2000DE-01019058.

07-APR-2000; 2000DE-01019173.

30-JUN-2000; 2000DE-01032529.

01-SEP-2000; 2000DE-01043826.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-602752/68.

Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.

Claim 1; SEQ ID NO 56; 27pp; English.

The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence is missing). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Seq Sequence 7667 BP; 2292 A; 63 C; 1436 G; 3876 T; 0 U; 0 Other;

Query Match 4.6%; Score 56.6; DB 4; Length 7667;

Best Local Similarity 46.9%; Pred. No. 0.021;

Matches 176; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 820 TATTCGCTCATGACTTTTCGTTAAATGATGTTTTTAAATAGTTATAACTTTTTTAG 879

DB 4585 TATTTTATGTTTATTTTAAATTTTATTTTAAATTTTATTTTATTTTGGTTAGATT 4644

QY 880 AACTATCTTCATTTAAATGATGATGACCTAGGTTTACATCATAGGAGTATCTGTTGAG 939

DB 4645 AGTTGTTTATTAATATATTAGTTATTTGTTTTTTTTTTTTTTTGTATTTTATAAG 4704

QY 940 CAATCATCATCTCGTTACTGATGGTCAACTACCCATATCAATATTTTATTAAGTCC 999

DB 4705 GTTTGTTTATGTTTATTTGTTGAGTTTCTGATTTTATTTTATTTGATTTATTTGATT 4764

QY 1000 CATCTCGAAAGTAATCCACATATCAGCTCTATTAAATCTGATCCTTCTTCATCTAATG 1059

DB 4765 TTTAAGTAGTTTTTATTGATTGTTTGTGTTAATTTTATTTTATTTTATTTTCTT 4824

QY 1060 TTAATTTTCCCTTTTTCGCGGTATCCATACCTGTTAAATGAATGTTTAAATCACTGTTT 1119

DB 4825 TTAATAATAGTATTTTTTTTGTATTTTGTGTAAGTGATTTTTTATTTATTAATTT 4884

QY 1120 TTGTGAGAAAGATATCCTTTTTCGTTTAAATGACTGACATGATATCTTTATTTCTT 1179

DB 4885 TTTATTTTGAATATTTGTTGTTGTTTAAATTTTGAATTTGTTATATTTTATTTAT 4944

QY 1180 GTTTTCTTAAAGCA 1194

DB 4945 TTTTATTAATAAGA 4959

RESULT 13

ABL32267

ID ABL32267 standard; DNA; 6419 BP.

XX

AC ABL32267;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human immune system associated gene SEQ ID NO: 240.

XX

KW Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmologic; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200200928-A2.

XX

PD 03-JAN-2002.

XX

PF 02-JUL-2001; 2001WO-EP007537.

XX

PR 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

DR WPI; 2002-130909/17.

XX

PT Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.

PT

XX

PS Claim 1; SEQ ID NO 240; 32pp + Sequence Listing; German.

XX

CC The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention

CC

XX

SQ Sequence 6419 BP; 1565 A; 53 C; 1453 G; 3348 T; 0 U; 0 Other;

Query Match 4.5%; Score 55.6; DB 6; Length 6419;

Best Local Similarity 47.6%; Pred. No. 0.033;

Matches 195; Conservative 0; Mismatches 214; Indels 1; Gaps 1;

CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention
 XX
 SQ Sequence 14006 BP; 3278 A; 155 C; 3257 G; 7313 T; 0 U; 3 Other;

Query Match 4.5%; Score 55.6; DB 6; Length 14006;
 Best Local Similarity 47.0%; Pred. No. 0.038;
 Matches 172; Conservative 0; Mismatches 194; Indels 0; Gaps 0;

QY 819 TTATTCGCTCATGACATTTTCGTTTAAAGTATTTTAAATAGTTTATAAACTTTTAA 878
 Db 1995 TTTTATTTTTCGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2054
 QY 879 GAACATATCTTCATTTAAATGATAGTAGTAAAGGTTTACATCATTAGGAGTATCTGTGTA 938
 Db 2055 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2114
 QY 939 GCAATCATCACTCGTTTACTGTGATGCTGCACTACCCATATGAAATATTTTATAGTC 998
 Db 2115 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2174
 QY 999 CCATCTCGAAAGTAAATCCACATATCACAGTCTATTAAATCTGATCCTTCTCATCTAAT 1058
 Db 2175 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2234
 QY 1059 GTTAAATTTCTCTTTTGTGGCGTATCCATCTACTGTAAATGAAGTTTAAATCACTGTT 1118
 Db 2235 TTTTATTTTTCGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2294
 QY 1119 TTTGTGAGAAAGATATCCCTTTTGTGTTTAAATGACTCGACATGATATCTTTATTTCT 1178
 Db 2295 TTTTTCGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2354
 QY 1179 TGTGTTT 1184
 Db 2355 TTTTIT 2360

RESULT 15
 ABK31511
 ID ABK31511 standard; DNA; 47108 BP.
 XX
 AC ABK31511;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Signal transduction associated gene modified complementary DNA #177.
 XX
 KW Human; signal transduction associated gene; cytosine methylation state;
 KW CpG island; signal transduction associated disease; solid tumour; cancer;
 KW antitumour; cytostatic; mutant; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200200926-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-EP007472.
 XX
 PR 30-JUN-2000; 2000DE-01032529.
 PR 01-SEP-2000; 2000DE-01043826.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX

775 TGPAAGTGTCCCTGAATATATATAGTACAAAAGTCATGAGCTTATTCGCTCATGACT 834
 Db 1571 TTTTATTTTTCGATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTATTT 1630
 QY 835 TTTTCGTTTAAAGATTTTAAATAAGTTATAAAGCTTTTTPAGAAGTATCTTCATTAA 894
 Db 1631 TATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTATTT 1690
 QY 895 AATGATAGTACGTAAGGTTTACATCATTAGGAGTATCTGTTGAGCAATCA-TCACCTCG 953
 Db 1691 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTATTT 1750
 QY 954 TTACTGTGATGTCACATCCCATATGAAATATTTTATAAGTCCCATCTCGAAAGTA 1013
 Db 1751 TTATTTATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTATTTAT 1810
 QY 1014 ATCCACATATCACAGTCTATTAAATCTGATCCTTCTTCATCTAATGTTAAATTTCCVTT 1073
 Db 1811 TTATTTATGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTATTTAT 1870
 QY 1074 TTGCGGTATCCATCTGTTAATGAATGTTTTTAAATCATCTGTTTGTGAGAAAGATA 1133
 Db 1871 TTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTATTTATTTG 1930
 QY 1134 TCCTTTTGTGTTTAAATGACTCGACATGATATCTTTATTTCTGTTT 1183
 Db 1931 TTGTTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTGTGTT 1960

RESULT 14
 ABL33958
 ID ABL33958 standard; DNA; 14006 BP.
 XX
 AC ABL33958;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human immune system associated gene SEQ ID NO: 1931.
 XX
 KW Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antianemic; cytostatic; nootropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antirheumatic; antiarthritic; antididiabetic; antipsoriatic;
 KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200200928-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-EP007537.
 XX
 PR 30-JUN-2000; 2000DE-01032529.
 PR 01-SEP-2000; 2000DE-01043826.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2002-130909/17.
 XX
 PT Nucleic acid comprising fragment of chemically modified gene, useful for
 PT diagnosis and treatment of diseases associated with abnormal cytosine
 PT methylation.
 XX
 PS Claim 1; SEQ ID NO 1931; 32pp + Sequence Listing; German.
 XX
 CC The present invention provides a number of human immune system associated

DR	WPI; 2002-147896/19.
XX	
PT	Oligonucleotide for diagnosis and therapy of diseases associated with
PT	signal transduction e.g. cancer, comprises chemically modified genomic
PT	sequences of genes associated with signal transduction.
XX	
PS	Claim 1; SEQ ID NO 354; 24pp; English.
XX	
CC	The present invention relates to chemically modified DNA sequences of
CC	signal transduction associated genes. The DNA sequences are chemically
CC	modified using a solution of bisulphite, hydrogen sulphite or disulphite.
CC	Also disclosed are oligonucleotides and/or PNA oligomers for detecting
CC	the cytosine methylation state (CpG islands) of these genes, and a method
CC	for the diagnosis and/or therapy of genetic and epigenetic parameters of
CC	genes associated with signal transduction. The genomic DNA can be
CC	obtained from cells or cellular components which contain DNA, e.g. cell
CC	lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid,
CC	tissue embedded in paraffin such as tissue from eyes, intestine, kidney,
CC	brain, heart, prostate, lung, breast or liver, histologic object slides,
CC	and all their possible combinations. The sequences of the invention are
CC	useful for the diagnosis and therapy of diseases associated with signal
CC	transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent
CC	chemically pretreated genomic DNA sequences of different genes associated
CC	with signal transduction, or their complementary sequences. Note: The
CC	sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from the
CC	European Patent Office
XX	
SQ	Sequence 47108 BP; 15349 A; 429 C; 8736 G; 22594 T; 0 U; 0 Other;
	Query Match 4.5%; Score 55.6; DB 6; Length 47108;
	Best Local Similarity 45.2%; Pred. No. 0.046;
	Matches 205; Conservative 0; Mismatches 249; Indels 0; Gaps 0;
QY	736 ATTTGGTTCCTTTTGACATCATATAGACGAGGAAGGGGATGTAAAGTGTTCCTCAATAT 795
Db	
	40450 ATGATATTTAAGGAACCGAATTTTAAATTTGGGGGTGTTTAATTAGTTGGTAGTGTA 40509
QY	796 ATATAGTACAAAAGTCATGAGCTTATTCGCCTCATGACTTTTTTCGTTTAAATGATTTTT 855
Db	
	40510 ATATTTTAAAAATTCGAAAAAATTTGGAAATTAAAAATTTTTTGGTTTAAAAAGTTTAGA 40569
QY	856 TAAATAAGTTATAAACCTTTTTTAGACTACTCTTCATTTAATTGATAGTACGTAAGTTTA 915
Db	
	40570 TAAGGTTATTTAAATTTGTATATAATTTTTTTTAAATGTTTAGTTATATATGATTTGATTA 40629
QY	916 CATCATTAGGAGTATCTTGTTCAGCAATCATCACTTCGTTACTGTGATGGTCACTACC 975
Db	
	40630 TATTTTATAAATATATTTTTTTTAAGTGTAAATGTTTAATGATATATATAAGATTA 40689
QY	976 ATATGAAATATTTTTATAGTCCCATCCTCGAAAGTAATCACATATCACAGTCTATTA 1035
Db	
	40690 ATGTAATATTTTTTTAAATATTTTAAAGATTTTTTGTGTGATATATTAATATTATTATT 40749
QY	1036 AATCTGATCCTTCTCATCTAATGTTAATTTTCCTTTTTTCGCCGTATCCATCTGTTAA 1095
Db	
	40750 TTTTAAAGTTTTTATATAAAAAATAAAAAATAATAGATGTTTTTGTGATGGAAATTTGTAG 40809
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	40810 TGGAGATTTTTTATTTGTTTGGTAGATTTTATGTTTTCGATTTTTTAAATTTTTTTTAAA 40869
QY	1156 CGACATGATATCTTTATTTCTTGTTTTTCTAA 1189
Db	
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Search completed: February 24, 2004, 02:43:29
Job time : 419 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 01:04:17 ; Search time 3429 Seconds
(without alignments)
15446.249 Million cell updates/sec

Title: US-10-019-661-1

Perfect score: 1222

Sequence: 1 ctttactgtattgttttatt.....tcatttgggtcttttgagt 1222

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

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12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

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34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1222	100.0	1222	1	AF196486	AF196486 Bacillus
2	1222	100.0	1222	6	AX068093	AX068093 Sequence
3	1037	84.9	1339	1	AF350927	AF350927 Bacillus
4	1037	84.9	1339	6	AX391415	AX391415 Sequence
C	1032.2	84.5	312049	1	AE017035	AE017035 Bacillus
C	1018.8	83.4	301665	1	AE017009	AE017009 Bacillus
7	980.2	80.2	1369	1	AY460124	AY460124 Bacillus
8	729	59.7	753	1	AF397400	AF397400 Bacillus
9	687.4	56.3	753	1	AF478058	AF478058 Bacillus
10	677.8	55.5	753	1	BAC505742	BAC505742 Unculture
11	644.2	52.7	753	1	AF350931	AF350931 Bacillus
12	644.2	52.7	753	6	AX391419	AX391419 Sequence
13	634.2	51.9	753	1	AF478052	AF478052 Bacillus
14	633.6	51.8	753	1	AF350930	AF350930 Bacillus
15	633.6	51.8	753	6	AX391418	AX391418 Sequence
16	633	51.8	753	1	AF478056	AF478056 Bacillus
17	628.2	51.4	753	1	AF195570	AF195570 Bacillus
18	625	51.1	753	1	AF478046	AF478046 Bacillus
19	625	51.1	753	1	AF478048	AF478048 Bacillus
20	625	51.1	753	1	AF478053	AF478053 Bacillus
21	625	51.1	753	1	AF478057	AF478057 Bacillus
22	623.4	51.0	753	1	AF350929	AF350929 Bacillus
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25	621.8	50.9	753	1	AF478045	AF478045 Bacillus
26	621.8	50.9	753	1	AF478050	AF478050 Bacillus
27	621.8	50.9	753	1	AF478059	AF478059 Bacillus
28	620.2	50.8	753	1	AF350928	AF350928 Bacillus
29	620.2	50.8	753	1	AF195571	AF195571 Bacillus
30	620.2	50.8	753	1	AY198412	AY198412 Bacillus
31	620.2	50.8	753	1	AX332611	AX332611 Bacillus
32	620.2	50.8	753	6	AX391416	AX391416 Sequence
33	618.6	50.6	753	1	AF478061	AF478061 Bacillus
34	617	50.5	753	1	AF350932	AF350932 Bacillus
35	617	50.5	753	1	AF350933	AF350933 Bacillus
36	617	50.5	753	1	AF478060	AF478060 Bacillus
37	617	50.5	753	6	AX391420	AX391420 Sequence
38	617	50.5	753	6	AX391421	AX391421 Sequence
39	615.4	50.4	753	1	AF350934	AF350934 Bacillus
40	615.4	50.4	753	1	AF478047	AF478047 Bacillus
41	615.4	50.4	753	1	AF478049	AF478049 Bacillus
42	615.4	50.4	753	6	AX391422	AX391422 Sequence
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44	613.8	50.2	753	1	AF478054	AF478054 Bacillus
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ALIGNMENTS

RESULT 1
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LOCUS AF196486
DEFINITION Bacillus sp. 240B1 putative metallohydrolase (aiia) gene, complete cds.
ACCESSION AF196486
VERSION AF196486.1 GI:7416988
KEYWORDS
SOURCE Bacillus sp. 240B1
ORGANISM Bacillus sp. 240B1
REFERENCE 1 (bases 1 to 1222)
AUTHORS Dong, Y.H., Xu, J.L., Li, X.Z. and Zhang, L.H.
TITLE AiiA, an enzyme that inactivates the acylhomoserine lactone quorum-sensing signal and attenuates the virulence of *Erwinia*

Pred. No. is the number of results predicted by chance to have a

JOURNAL	Carotovora
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3526-3531 (2000)
PUBMED	20202669
REFERENCE	10716724
AUTHORS	2 (bases 1 to 1222)
TITLE	Dong Y.-H., Xu J.-L. and Zhang L.-H.
JOURNAL	Direct Submission
	Submitted (20-OCT-1998) Institute of molecular Agrobiology, 1
	Research Link, The University of Singapore, Singapore 117604,
	Singapore
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ORIGIN	
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Best Local Similarity	100.0%; Pred. No. 4.7e-213;
Matches 1222; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Qy	61 AAGCTTTATTTTCGCCAGCAGGTCGTTGTATGTTGGATCATTCGTCGTGTTAAATGATACA 120
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Qy	121 TTAACACAGAGAAATTAATATAGACTTACC GGTTTGCGTTGTTATCTTTTGGAGACTGAAGAA 180
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Qy	181 GGACCTATTTTGTAGTATGATACAGGTATGCCAGAAAGTCAGTAAATTAATGAAGGTCCTTTT 240
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Qy	241 AACGGTACATTTGTCGAAGGCGCAGGTTTAC CGAAAATGACTGAAGAAGATAGATATCGTG 300
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Qy	301 AATATTTTAAACCGGTTGTTATGACGCGGAGACCTTCCTTATATTATTAGTTCTCCAC 360
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Qy	301 AATATTTTAAACCGGTTGTTATGACGCGGAGACCTTCCTTATATTATTAGTTCTCCAC 360
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Qy	361 TTGCATTTTGTATCATGCAAGGAGAAATGGCGCTTTTATAAAATACACCAATCATTTGTACAG 420
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Qy	361 TTGCATTTTGTATCATGCAAGGAGAAATGGCGCTTTTATAAAATACACCAATCATTTGTACAG 420
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Qy	421 CGTGCTGAATATGAGCGCGGCGCAGCATAGCGNAGATATTTGARAAGATGTATATTGCGG 480
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Qy	421 CGTGCTGAATATGAGCGCGGCGCAGCATAGCGNAGATATTTGARAAGATGTATATTGCGG 480
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Qy	481 AATTTAAACTACAAAAATCATTTGAAGTGCAATTATGAAGTCGTACACAGGAGTTCAATTATTG 540
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Qy	481 AATTTAAACTACAAAAATCATTTGAAGTGCAATTATGAAGTCGTACACAGGAGTTCAATTATTG 540
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Qy	541 CATACACAGGCGCATCTCCAGGGONCATCGCTATTAAATTGACACAGAAAAATCCGGT 600

Best Local Similarity 100.0%; Pred. No. 4.7e-213; Matches 1222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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QY	121	TTAACACACAGAGATTAATAGACTTACCGGTTTGGTGTATCTTTGGAGACTGAAGAA	180
Db	121	TTAACACACAGAGATTAATAGACTTACCGGTTTGGTGTATCTTTGGAGACTGAAGAA	180
QY	181	GGACCTATTTTAGTAGATACAGGTATGCCAGAACTGCAGTTAAATAAGAGGTCCTTTT	240
Db	181	GGACCTATTTTAGTAGATACAGGTATGCCAGAACTGCAGTTAAATAAGAGGTCCTTTT	240
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QY	301	AATATTTTAAACCGGTTGGTTATGAGCGGGAAGACCTTCTTTATATTTAGTCTCAC	360
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QY	421	CGTGCTGAATANGCGGCGGCGACATAGCGAAGAATATTTGAAAGAAATGTATATTGCGG	480
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QY	481	AATTTAAACTACAAAATCATTTGAAGGTGATTTGAAGTCGTACAGAGTTCAATTTATG	540
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QY	541	CATACACAGGCCATATCCAGGCGCATCAATCGCTATTAATGAGACAGAAAATCCGGT	600
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QY	661	TTTTCGGGATTTGATTCAGAAATGCTTTTATCTTCAATTAACGTTTAAAGAAAGTCGGT	720
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QY	721	ATGAAGAGAGAGCGGATTTGTTTCTTTGGACATGATAGACAGGAAAGGGGATGTAAA	780
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QY	841	TTTTAAATGATTTTTTAAATAGTATAAACTTTTTTTAGAACTATCTTCAATTTAATGTAT	900
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Qy	1201	GCTCATTTGGGTCTCTTTGAGT	1222
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LOCUS	AF350927	1339 bp	DNA linear BCT 28-MAR-2002
DEFINITION	Bacillus sp. COT1 AHL-lactonase (aiaA-COT1) gene, complete cds.		
ACCESSION	AF350927		
VERSION	AF350927.1	GI:19773592	
KEYWORDS			
SOURCE	Bacillus sp. COT1		
ORGANISM	Bacillus sp. COT1		
REFERENCE	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
AUTHORS	1 (bases 1 to 1339)		
TITLE	Dong, Y.H., Gusti, A.A., Xu, J.L. and Zhang, L.H.		
JOURNAL	Identification of quorum-quenching N-acyl homoserine lactonases from Bacillus species		
MEDLINE	Appl. Environ. Microbiol. 68 (4), 1754-1759 (2002)		
REFERENCE	21914084		
AUTHORS	2 (bases 1 to 1339)		
TITLE	Dong, Y.H., Gusti, A.A., Xu, J.L. and Zhang, L.H.		
JOURNAL	Direct Submission		
FEATURES	Submitted (21-FEB-2001) Institute of Molecular Agrobiolgy, The National University of Singapore, 1 Research Link, Singapore 117604		
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Qy	122	TACACCCAGAGAAATTTAGACTTACCCTGTTGGTGTATCTTTTGGAGACTGAAGAAG	181

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Db 1319 CTCATTTGGATCCCTTTGAGT 1339

RESULT 4
AX391415 1339 bp DNA linear PAT 23-MAR-2002
LOCUS Sequence 2 from Patent WO0216623.
DEFINITION
ACCESSION AX391415
VERSION AX391415.1 GI:19700038
KEYWORDS
SOURCE
ORGANISM
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
1 Zhang, L., Dong, Y. L. and Xu, J.
Bacterial strains, genes and enzymes for control of bacterial diseases by quenching quorum-sensing signals
Patent: WO 0216623-A 2 28-FEB-2002;
Institute of Molecular Agrobiolology (SG)

FEATURES
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166 918
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ORIGIN
Query Match 84.9%; Score 1037; DB 6; Length 1339;
Best Local Similarity 90.6%; Pred. No. 2.5e-179;
Matches 1106; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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LOCUS			
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	Bacillus anthracis str. Ames	section 12 of 18 of the complete	
genome.			
ACCESSION	AE017035	AE016879	
VERSION	AE017035.1	GI:30258016	
KEYWORDS			
SOURCE			
ORGANISM			
	Bacillus anthracis str. Ames		
	Bacillus anthracis str. Ames		
	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus		
	cereus group.		
REFERENCE			
AUTHORS			
	1 (bases 1 to 312049)		
	Read, T., Peterson, S., Tourasse, N., Baillie, L., Paulsen, I.,		
	Nelson, K., Tettelin, H., Fouts, D., Eisen, J., Gill, S., Holtzapple, E.,		
	Okstad, O., Helgason, E., Rilstone, J., Wu, M., Kolonay, J., Beanan, M.,		
	Dodson, R., Brinkac, L., Gwinn, M., DeBoy, R., Madupu, R., Daugherty, S.,		
	Durkin, A., Haft, D., Nelson, W., Peterson, J., Pop, M., Khouri, H.,		
	Radune, D., Benton, J., Mahamoud, Y., Jiang, L., Hance, I., Weidman, J.,		
	Berry, K., Plaut, R., Wolf, A., Watkins, K., Nierman, W., Hazen, A.,		
	Cline, R., Redmond, C., Thwaite, J., White, O., Salzberg, S.,		
	Thomason, B., Friedlander, A., Koehler, T., Hanna, P., Kolsto, A.-B. and		
	Fraser, C.		
TITLE			
	The genome sequence of Bacillus anthracis Ames and comparison to		
	closely related bacteria		
JOURNAL			
MEDLINE			
	Nature 423 (6935), 81-86 (2003)		
	22608414		
12721629			
2 (bases 1 to 312049)			
Read, T., Peterson, S., Tourasse, N., Baillie, L., Paulsen, I.,			
Nelson, K., Tettelin, H., Fouts, D., Eisen, J., Gill, S., Holtzapple, E.,			
Okstad, O., Helgason, E., Rilstone, J., Wu, M., Kolonay, J., Beanan, M.,			
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Durkin, A., Haft, D., Nelson, W., Peterson, J., Pop, M., Khouri, H.,			
Radune, D., Benton, J., Mahamoud, Y., Jiang, L., Hance, I., Weidman, J.,			
Berry, K., Plaut, R., Wolf, A., Watkins, K., Nierman, W., Hazen, A.,			
Cline, R., Redmond, C., Thwaite, J., White, O., Salzberg, S.,			
Thomason, B., Friedlander, A., Koehler, T., Hanna, P., Kolsto, A.-B. and			
Fraser, C.			
Direct Submission			
Submitted (26-MAR-2003) The Institute for Genomic Research, 9712			
Medical Center Dr, Rockville, MD 20850, USA			
Location/Qualifiers			
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RESULT 6
AE017009/c 301665 bp DNA linear BCT 16-MAY-2003
LOCUS Bacillus cereus ATCC 14579 section 12 of 18 of the complete genome.
DEFINITION AE017009 AE016877
ACCESSION AE017009.1 GI:29897026
VERSION
KEYWORDS
SOURCE
ORGANISM
Bacillus cereus ATCC 14579
Bacillus cereus ATCC 14579
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE
1 (bases 1 to 301665)
AUTHORS
Ivanova,N., Sorokin,A., Anderson,I., Galleron,N., Candelon,B.,
Kapatral,V., Bhattacharya,A., Reznik,G., Mikhailova,N.,
Lapidus,A., Chu,L., Mazur,M., Goitsman,E., Larsen,N., D'Souza,M.,
Walunas,T., Grechkin,Y., Pusch,G., Haselkorn,R., Fonstein,M.,
Ehrlich,D.S.D., Overbeek,R. and Kyrpides,N.
Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis
JOURNAL Nature 423 (6935), 87-91 (2003)
MEDLINE 22608415
PUBMED 12721630
REFERENCE
2 (bases 1 to 301665)
AUTHORS
Candelon,B., Galloux,K., Ehrlich,D.S. and Sorokin,A.
TITLE The number of ribosomal RNA operons in Bacillus cereus
JOURNAL Unpublished
REFERENCE
3 (bases 1 to 301665)
```

AUTHORS

Ivanova,N., Sorokin,A., Anderson,I., Galleron,N., Candelon,B., Kapatral,V., Bhattacharya,A., Reznik,G., Mikhailova,N., Lapidus,A., Chu,L., Mazur,M., Goitsman,E., Larsen,N., D'Souza,M., Walunas,T., Grechkin,Y., Pusch,G., Haselkorn,R., Fonstein,M., Ehrlich,D.S.D., Overbeek,R. and Kyrpides,N.
Direct Submission
Submitted (12-MAR-2003) INRA, Genetique Microbienne, Domaine de Vilvert, Jouy en Josas 78352, France
Location/Qualifiers
1. 301665

TITLE
JOURNALFEATURES
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KEYWORDS

SOURCE Bacillus thuringiensis serovar toumanoffii
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 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE

1 (bases 1 to 753)
 Lee, S.-J., Park, S.-Y., Lee, J.-J., Yum, D.-Y., Koo, B.-T. and Lee, J.-K.
 Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
 Widespread in Many Subspecies of *Bacillus thuringiensis*
 Appl. Environ. Microbiol. 68 (8), 3919-3924 (2002)

JOURNAL

PUBMED 12147491

AUTHORS

2 (bases 1 to 753)
 Lee, S.-J., Park, S.-Y., Yum, D.-Y. and Lee, J.-K.

TITLE

Direct Submission

JOURNAL

Submitted (30-JAN-2002) R&D Center, inBionet Corporation,
 Jommin-dong 461-6, Yusong, Deajeon 305-390, Korea

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 VERSION AJ505742.1
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 ORGANISM uncultured Bacillus sp.
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 environmental samples.
 REFERENCE 1
 AUTHORS Carlier, A., Uroz, S., Smadja, B., Fray, R., Latour, X., Dessaux, Y. and
 Faure, D.
 TITLE The π Plasmid of *Agrobacterium tumefaciens* Harbors an
 atM-Paralogous Gene, aiiB, Also Encoding N-Acyl Homoserine
 Lactonase Activity
 JOURNAL Appl. Environ. Microbiol. 69 (8), 4989-4993 (2003)
 MEDLINE 22783888
 PUBMED 12902298
 REFERENCE 2 (bases 1 to 753)
 AUTHORS Fray, R.G.
 TITLE Direct Submission
 JOURNAL Submitted (12-AUG-2002) Fray R.G., School of Biosciences,
 University of Nottingham, Sutton Bonington Campus, Loughborough,
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Zhang, J., Dong, Y. L. and Xu, J.
Bacterial strains, genes and enzymes for control of bacterial
diseases by quenching quorum-sensing signals
Patent: WO 0216623-A 6 28-FEB-2002;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
1 (bases 1 to 753)
Lee, S.-J., Park, S.-Y., Lee, J.-J., Yum, D.-Y., Koo, B.-T. and Lee, J.-K.
Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
Widespread in Many Subspecies of Bacillus thuringiensis
Appl. Environ. Microbiol. 68 (8), 3919-3924 (2002)
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2 (bases 1 to 753)
Lee, S.-J., Park, S.-Y., Yum, D.-Y. and Lee, J.-K.
Direct Submission
Submitted (30-JAN-2002) R&D Center, inBionET Corporation,
Jonmin-dong 461-6, Yusong, Daejeon 305-390, Korea
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DEFINITION Sequence 5 from Patent WO0216623.

ACCESSION AX391418

VERSION AX391418.1 GI:19700041

KEYWORDS Bacillus thuringiensis

SOURCE Bacillus thuringiensis

ORGANISM Bacillus thuringiensis

REFERENCE 1

AUTHORS Zhang L., Dong, Y.L. and Xu, J.

TITLE Bacterial strains, genes and enzymes for control of bacterial diseases by quenching quorum-sensing signals

JOURNAL Patent: WO 0216623-A 5 28-FEB-2002;

INSTITUTE Institute of Molecular Agrobiolology (SG)

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Copyright (c) 1993 - 2004 CompuGen Ltd.

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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11	107	8.1	211	1 YQGX_BACSU	P34501 bacillus su
12	106.5	8.1	215	1 YCBL_ECOLI	Q57744 methanococc
13	105.5	8.0	281	1 YND2_YEAST	P53965 saccharomyc
14	100.5	7.6	258	1 GL2C_ARATH	Q24496 arabidopsis
15	99.5	7.6	220	1 YVBB_BACSU	P37502 bacillus su
16	96	7.3	474	1 C1SY_EMENI	Q00098 emericella
17	96	7.3	610	1 GIDA_CHLMU	Q9pjp3 chlamydia m
18	95.5	7.3	479	1 C1SY_YEAST	P00890 saccharomyc
19	94.5	7.2	319	1 YQJP_BACSU	P54553 bacillus su
20	94.5	7.2	543	1 Y274_METJA	Q57722 methanococc
21	94	7.1	475	1 C1SY_ASPNG	P51044 aspergillus
22	93.5	7.1	250	1 GLO2_BUCAP	Q08889 buchnera ap
23	92	7.0	1609	1 YL54_CAEEL	P34434 caenorhabdi
24	91	6.9	260	1 GLO2_HUMAN	Q16775 homo sapien
25	90.5	6.9	706	1 SM2A_DROME	Q24323 drosophila
26	90.5	6.9	4427	1 PKSL_BACSU	Q05470 bacillus su
27	90	6.8	251	1 GLO2_BUCAI	P57336 buchnera ap
28	89	6.8	254	1 BLAB_AERYH	P26918 aeromonas h
29	89	6.8	294	1 X301_METJA	P57749 methanococc
30	89	6.8	1018	1 FNBA_STAAU	P14738 staphylococ
31	88.5	6.7	260	1 GLO2_CALJA	Q28333 callithrix
32	87.5	6.7	383	1 DGT1_RICPR	Q9ze82 rickettsia
33	87.5	6.7	421	1 Y162_METJA	Q57626 methanococc

34	87	6.6	448	1 Y861_METJA	Q58271 methanococc
35	86.5	6.6	256	1 Y448_METJA	Q57890 methanococc
36	86.5	6.6	285	1 GLO4_YEAST	Q12320 saccharomyc
37	86.5	6.6	1104	1 BUD2_YEAST	P33314 saccharomyc
38	86.5	6.6	1181	1 ITA2_HUMAN	P17301 homo sapien
39	86	6.5	371	1 CARA_PYRFU	Q8u086 pyrococcus
40	86	6.5	404	1 FFAA_METTM	Q50497 methanobact
41	85.5	6.5	434	1 ENO_STAEP	Q8cpj3 staphylococ
42	85.5	6.5	449	1 TL40_SPIOL	Q49939 spinacia ol
43	85	6.5	356	1 YXT2_CAEEL	Q18078 caenorhabdi
44	85	6.5	612	1 MCR_XENLA	Q91573 xenopus lae
45	85	6.5	637	1 GYRE_TREPA	O08399 treponema p

ALIGNMENTS

RESULT 1
YN00_MYCTU
ID YN00_MYCTU STANDARD; PRT; 310 AA.
AC Q50665;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein Rv2300c.
GN Rv2300c OR MT2357 OR MTCY339.09.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulten J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; Z77163; CAB00971.1; --
CC EMBL; AE007078; AA46642.1; --
CC PIR; H70733; H70733.
CC TIGR; MT2357; --
CC Tuberculist; Rv2300c; --
CC InterPro; IPR001279; Blackmase-like.
CC Pfam; PF00753; lactamase_B; 1.
CC Hypothetical protein; Complete proteome.
KW

Tue Feb 24 12:13:12 2004

SEQ SEQUENCE 310 AA; 34352 MW; 0764F4FA64AB5E51 CRC64;
 Query Match 11.9%; Score 157; DB 1; Length 310;
 Best Local Similarity 25.7%; Pred. No. 4.9e-06;
 Matches 62; Conservative 34; Mismatches 87; Indels 58; Gaps 11;

QY	39	LLETGSGPILVDTGM-----PESAVNREGLFNGTFVEGVLPKMTTEDRIVNLKRVG 91
Dd	74	LVTETDGLVLNDTGFQIDCLDP-----GRVGLFRHV-----LRPAFLQAETAARQIEQLG 124
QY	92	YRPEDLYLISSHLHFDHAGNGAFINTRIIVQRAEYEAASHSEYLKECILPNLNY--- 148
Dd	125	YRTSDVRHVLVTHFDHDHGIGADFFPEAHLVHTAAEARGAIHAPS-LRE----RLRYRRG 179
QY	149	-----KLIEGDYEVPV-----GVOLLTPGHTPGHOSLLIETEKSGPVL 187
Dd	180	QWAHGPVKLVHEGPDGEWRGFSASAKPLDSIGTGVLVPMFGHTRGHAAVAVDAGRHW-VL 238
QY	188	LTTDASYTKENFEN--EVPAGEDSELALS-----SIKRLKVVMKEXP--IVFPGH 235
Dd	239	HCGDAFYHRGTLDGRFRFPVFMRAEEKLSVNRNLQNQRARVELHRHPDLLIVCAH 298
QY	236	D 236
Dd	299	D 299

RESULT 2
 Y296 METJA STANDARD; PRT; 203 AA.
 ID_Y296 METJA
 AC Q57744;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJ0296.
 GN MJ0296
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcaceae;
 NCBI_TaxID=2190;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=9688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kervilange A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.F.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, *Methanococcus*
 RL *jannaschii*";
 CC Science 273:1058-1073(1996).
 CC -!- SIMILARITY: WEAK, TO M.JANNASCHII MJ0888.

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CC	EMBL; U67484; AAB98284.1; --
DR	PIR; A64337; A64337.
DR	TIGR; MJ0296; --
DR	InterPro; IPR001279; Blactmase-like.
DR	Pfam; PF00753; lactamase_B; 1.
SQ	Hypothetical protein; Complete proteome.
KW	SEQUENCE 203 AA; 23236 MW; 9039A9CB6F9E75D CRC64;

DE Hypothetical protein MJ0047.
GN MJ0047.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -I- SIMILARITY: STRONG TO M.JANNASCHII MJ0162 AND MJ1236. ALSO
CC SIMILAR TO SYNECHOCYSTIS PCC 6803 SLL0514.
CC
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CC
CC EMBL; U67462; AAB98027.1; -.
CC TIGR; MJ0047; -.
DR InterPro; IPR001279; Blactmase-like.
DR Pfam; PF00753; lactamase_B; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 428 AA; 48492 MW; A649ED66705AA01B CRC64;

Query Match 8.8%; Score 115.5; DB 1; Length 428;
Best Local Similarity 20.8%; Pred. No. 0.025;
Matches 51; Conservative 44; Mismatches 73; Indels 77; Gaps 10;

Qy 28 GELLDPVWCYLLTEGPIIVDPMPESAVNNEGLFNGFVGEQVLPKMTEDRIUNIL 87
Db 7 GAALVGRSGTEIKTKSKILLDCGVK-----LGKEIEYPILDNSI 47

Qy 88 KRVCYEPEDLLYLISSHLFHDHAGNGAF---INTPLI-----VQR 125
Db 48 RDV-----DKVFI--SHALHDHGALPVLFRKMDVPVITTELSKKLIKVLKDMVKIAE 100

Qy 126 AVEEAAQHSBEYLKECI---LP-NLNYKIIIEGDEYVPGVQLLTPGHTPGHQSLLIETE 181
Db 101 TENKKIPYNNHDVKEAIRHTIPLNVDNKKYKDFSYE-----LFSAGHIPGSASILLNYQ 155

Qy 182 KSGPVILT-----IDASYKENPENEVPFAGFSEI-----ALSIRKLK 221
Db 156 NNKTIYTGDKVLRDTRLTGKADLSYTKDDILIIESTYGNISHPDKAVELSFIEKIK 215

Qy 222 EVVMK 226
Db 216 EILFR 220

RESULT 6
GL2M ARATH
ID GL2M ARATH STANDARD; PRT; 331 AA.
AC O24495; O22857; O24494;
DT 15-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hydroxycyglutathione hydrolase, mitochondrial precursor (EC 3.1.2.6)
DE (Glyoxalase II) (Glx II).

GN GLX2-1 OR AT2G43430 OR TIO24.17
OS Arabidopsis thaliana (Mouse-ear cress).
OC Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wassilewskija;
RX MEDLINE=98009983; PubMed=9349270;
RA Maiti M.K., Krishnasamy S., Owen H.A., Makaroff C.A.;
RT "Molecular characterization of glyoxalase II from Arabidopsis
RT thaliana.";
RL Plant Mol. Biol. 35:471-481(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Renning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Niernan W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAPs) sequenced by the
RT SRP consortium (Salk/Stanford/PGEC).";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: THIOLESTERASE THAT CATALYZES THE HYDROLYSIS OF S-D-
CC LACTOYL-GLUTATHIONE TO FORM GLUTATHIONE AND D-LACTIC ACID.
CC -I- CATALYTIC ACTIVITY: (S)-(2-hydroxyacyl)glutathione + H(2)O =
CC Glutathione + a 2-hydroxy acid anion.
CC -I- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
CC -I- PATHWAY: Glyoxal pathway.
CC -I- SUBCELLULAR LOCATION: Mitochondrial.
CC -I- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U90927; AAC49865.1; -.
CC EMBL; U90928; AAC49866.1; -.
DR EMBL; AC002335; AAB64315.2; -.
DR EMBL; AY091278; AAM14217.1; -.
DR EMBL; AY063806; AAL36162.1; -.
DR HSSP; Q16775; 1QH5.
DR InterPro; IPR001279; Blactmase-like.
DR Pfam; PF00753; lactamase_B; 1.
KW Hydrolase; Zinc; Mitochondrion; Transit peptide.
FT TRANSIT 1 76 MITOCHONDRION (POTENTIAL).
FT CHAIN 77 331 HYDROXYCYGLUTATHIONE HYDROLASE.
FT METAL 131 131 ZINC 1 (BY SIMILARITY).
FT METAL 133 133 ZINC 1 (BY SIMILARITY).
FT METAL 135 135 ZINC 2 (BY SIMILARITY).
FT METAL 136 136 ZINC 2 (BY SIMILARITY).
FT METAL 189 189 ZINC 1 (BY SIMILARITY).
FT METAL 208 208 ZINC 1 AND 2 (BY SIMILARITY).
FT METAL 159 159 D -> H (IN REF. 1; AAC49866).
SQ SEQUENCE 331 AA; 36499 MW; 2EDC21B4902419C5 CRC64;

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EMBL; X75074; CAA52968.1; -
PDB; 1SML; 20-SEP-99.
InterPro; IPR001018; Beta lactamase B.
InterPro; IPR001279; Blactamase-like.
Pfam; PF00753; lactamase B; 1.
PROSITE; PS00743; BETA LACTAMASE B.1; 1.
PROSITE; PS00744; BETA LACTAMASE B.2; FALSE NEG.
Hydrolase; Zinc; Antibiotic resistance; Periplasmic; Signal;
3D-structure. 1 21 POTENTIAL.
SIGNAL 22 33
PROPEP 22 33
CHAIN 34 290 METALLO-BETA-LACTAMASE L1.
DISULFID 239 267
METAL 105 105 ZINC 1.
METAL 107 107 ZINC 1.
METAL 109 109 ZINC 2.
METAL 181 181 ZINC 1.
METAL 205 205 ZINC 2.
METAL 217 217 ZINC 2.
CONFLICT 36 37 AS -> QR (IN REF. 2).
CONFLICT 40 40 Q -> A (IN REF. 2).
CONFLICT 56 58 TED -> ROH (IN REF. 2).
CONFLICT 63 63 L -> H (IN REF. 2).
HELIX 36 39
STRAND 41 41
STRAND 45 48
TURN 49 50
STRAND 51 53
STRAND 56 56
TURN 57 58
STRAND 59 59
STRAND 62 66
TURN 67 68
STRAND 69 73
STRAND 76 76
HELIX 78 80
HELIX 81 90
TURN 91 92
HELIX 95 97
STRAND 98 102
HELIX 108 111
TURN 112 113
HELIX 114 120
STRAND 124 127
HELIX 129 136
TURN 137 139
STRAND 142 142
TURN 143 145
STRAND 146 146
TURN 147 147
STRAND 158 159
TURN 162 163
STRAND 165 168
TURN 169 170
STRAND 171 177
TURN 183 184
STRAND 186 194
TURN 195 196
STRAND 197 203
TURN 210 211
TURN 218 219
TURN 221 222
HELIX 223 235
TURN 236 236
STRAND 241 243
HELIX 247 250
TURN 251 251

Matches 51; Conservative 29; Mismatches 56; Indels 71; Gaps 11;
QY 79 EEDRIVNLRKRGVPEPDLIIYISSHLPHDAGNGAFINTPIIVORAEYAAQH-----133
Db 33 EAERLIQRTEELDL---NLKVLTLTHGLDHVG-----AAMQLKQHPGVVEI 75
QY 134 -----SEEVKQCI-----LPNLYKI-----IEGDYEVVPG--VQLLHTPGHTG 172
Db 76 WGSNEKDKLFESLPQAOQFGLNIDAFLPDRWFNQEGEILKLDGTFNFIHLPGHTG 135
QY 173 HQSLLETSGEVLITIDASYTKENFENEVPAG-----PSELALSISIKELKEV 223
Db 136 HIG-FIEHEK-----KVAFTGDVLFQGGIGRTDPPRGDYETLISSI-RTKLL 180
QY 224 VMKEKPIVFVFGH-----DIEQERGCKVF 246
Db 181 PLNDIIIIAGHSGSYTTIGQEKSNPF 207
RESULT 9
BLA1_XANMA STANDARD; PRT; 290 AA.
AC P52700;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Metallo-beta-lactamase L1 precursor (Beta-lactamase, type II)
DE (EC 3.5.2.6) (penicillinase).
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Stenotrophomonas.
OX NCBI_TaxID=40324;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IID 1275.
RX MEDLINE=94289479; PubMed=8018721;
RA Walsh T.R., Hall L., Assinder S.J., Nichols W.W., Cartwright S.J.,
RA Macgowan A.P., Bennett P.M.;
RT "Sequence analysis of the L1 metallo-beta-lactamase from Xanthomonas maltophilia";
RL Biochim. Biophys. Acta 1218:199-201(1994).
RN [2]
RP SEQUENCE OF 34-65.
RC STRAIN=IID 1275;
RX MEDLINE=86025393; PubMed=3931629;
RA Bicknell R., Emanuel E.L., Gagnon J., Waley S.G.;
RT "The production and molecular properties of the zinc beta-lactamase of Pseudomonas maltophilia IID 1275";
RL Biochem. J. 229:791-797(1985).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX MEDLINE=99030465; PubMed=9811546;
RA Ullah J.H., Walsh T.R., Taylor I.A., Emery D.C., Verma C.S.,
RA Gamblin S.J., Spencer J.;
RT "The crystal structure of the L1 metallo-beta-lactamase from Stenotrophomonas maltophilia at 1.7 A resolution";
RL J. Mol. Biol. 284:125-136(1998).
CC 1- FUNCTION: HAS A HIGH ACTIVITY AGAINST IMPENEM. UNSTABLE BELOW PH 8. UNLESS ZINC IS PRESENT.
CC 1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-amino acid.
CC 1- COFACTOR: BINDS TWO ZINC IONS PER MOLECULE.
CC 1- ENZYME REGULATION: Inhibited by Hg(2+) or Cu(2+). Reduced enzymatic activity in presence of Co(2+), Ni(2+), Cd(2+), and Mn(2+).
CC 1- SUBUNIT: Homotetramer.
CC 1- SUBCELLULAR LOCATION: Periplasmic (Potential).
CC 1- SIMILARITY: Belongs to the class-B beta-lactamase family.
CC
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FT HELIX 254 259
FT TURN 260 263
FT HELIX 267 287
SQ SEQUENCE 290 AA; 30801 MW; 0B34CAB54518BC1E CRC64;

Query Match 8.4%; Score 110.5; DB 1; Length 290;
Best Local Similarity 21.5%; Pred. No. 0.039;
Matches 40; Conservative 30; Mismatches 57; Indels 59; Gaps 7;

QY 39 LLETEEGPILVDTPGPEAVNNEGLFNGFTVEGVQLPKQWEDRIVNILKRVGVEPEDLL 98
Db 63 LVQPDGAVLLDGGMPQMA-----SHLLDNMKARGVTPRDLR 99
QY 99 YIISHLHFDHAGNGAFINPTI--IVQRAEYEAQHSEYILKBCIL----- 143
Db 100 LILLSHAHADHAG-----PVALKRRTGAKVAANA-----SAVLLARGSGDDLLHFGD 147
QY 144 -----PNLNKIIIEGDEYVVGQVQL--HTFGHTPGHQS--LLIETKSGPVLITIDASY 194
Db 148 GITPPANADRIVMDEGITVGGIVFTAHFVAGHTPGSTAWTWTDRNGKPVRIAYADSL 207
QY 195 TKNFPE 200
Db 208 SAPGYQ 213

RESULT 10
GLO2_YEAST STANDARD; PRT; 274 AA.
AC Q05584;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hydroxyacylglutathione hydrolase, cytoplasmic isozyme (EC 3.1.2.6)
DE (Glyoxalase II) (Glx II).
GN GLO2 OR YDR272W OR D9954.5.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W303;
RX MEDLINE=97407946; PubMed=9261170;
RA Bito A., Haider M., Hadler I., Breitenbach M.;
RT "Identification and phenotypic analysis of two glyoxalase II encoding
RT genes from Saccharomyces cerevisiae, GLO2 and GLO4, and intracellular
RT localization of the corresponding proteins.";
RL J. Biol. Chem. 272:21509-21519(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnson L., Langston Y., Latreille P., Le T.,
RA Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Rifken L., Riles L., Taich L., Trevisan E., Vignati D.,
RA Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Thiolesterase that catalyzes the hydrolysis of S-D-
CC lactoyl-glutathione to form glutathione and D-lactic acid.
CC CC -1- CATALYTIC ACTIVITY: (S)-(2-hydroxyacyl)glutathione + H(2)O =
CC glutathione + a 2-hydroxy acid anion.
CC CC -1- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
CC CC -1- PATHWAY: Glyoxal pathway.
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC CC -1- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
CC -----
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EMBL; Y10292; CAA71335.1; -.
 DR EMBL; U51030; AAB64450.1; -.
 DR PIR; S70130; S70130.
 DR HSSP; Q16775; 1QH5.
 DR SGD; S0002680; GLO2.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0004416; F:hydroxyacylglutathione hydrolase activity; IMP.
 DR GO; GO:0005975; P:carbohydrate metabolism; IMP.
 DR InterPro; IPR001279; Blackmase-like.
 DR Pfam; PF00753; lactamase B; 1.
 DR Hydrolase; Zinc; Multigene family.
 FT METAL 59 59 ZINC 1 (BY SIMILARITY).
 FT METAL 61 61 ZINC 1 (BY SIMILARITY).
 FT METAL 63 63 ZINC 2 (BY SIMILARITY).
 FT METAL 64 64 ZINC 2 (BY SIMILARITY).
 FT METAL 121 121 ZINC 1 (BY SIMILARITY).
 FT METAL 144 144 ZINC 1 AND 2 (BY SIMILARITY).
 FT METAL 188 188 ZINC 2 (BY SIMILARITY).
 SQ SEQUENCE 274 AA; 31326 MW; 6CD7AB9F0A9399EA CRC64;

Query Match 8.3%; Score 109.5; DB 1; Length 274;
 Best Local Similarity 21.8%; Pred. No. 0.044;
 Matches 50; Conservative 40; Mismatches 82; Indels 57; Gaps 11;
 QY 36 WCYLLETEEG--PILVDTPGPEAVNNEGLFNGFTVEGVQLPKQWEDRIVNILKRVGYE 93
 Db 17 YCILLSDSKNKKSWLIDPAEPP-----EVLPELDEKIL----- 50
 QY 94 PEDLYIITSSHLHFDHAGNGAFI-----NTPIIQVRAEYEAQHSEYILKBCILPNLNY 148
 Db 51 --SVEAIWNTHHYDHADGNADILKYLKNP---TSKVEVIGSGKDCPKVTIIPENLK 104
 QY 149 KILEGDEYVVGQVQLLHPTGHTPGHQSLLIETKSGP-VLLITIDASYTK--ENFENEVPP 205
 Db 105 KLHLGDLLEIT---CIRTPCHTRDSICYVYKDPPTTDERCIFTGDTLFTAGCGRP---F 155
 QY 206 AGFDSSELALSSIKRLKEVNMKE---KPIVFFGHDIQER---GCKVFPE 248
 Db 156 EGIGEMDIANNSILETVGRQNSKTRVTPGHEYTSNPKVFRKIYPQ 204

RESULT 11
 YQGX_BACSU STANDARD; PRT; 211 AA.
 ID YQGX_BACSU STANDARD; PRT; 211 AA.
 AC P3450L; 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein yqgx.
 GN YQGX.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / JH642;
 RX MEDLINE=97124195; PubMed=8969508;
 RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
 RA Kobayashi Y.;
 RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
 RT the Bacillus subtilis genome containing the skin element and many
 RT sporulation genes.";
 RL Microbiology 142:3103-3111(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrai E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haech J., Harwood C.R., Henaut A.,
RA Hilbert H., Hollappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koeter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel J., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serron P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Taseuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -!- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
CC
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CC
CC EMBL; D84432; BAA12527.1; --
CC EMBL; Z99116; CAB14410.1; --
CC PIR; A69958; A69958.
CC Subtilisin; BG11691; YggX.
DR InterPro; IPR001279; Blactamase-like.
DR Pfam; PF00753; lactamase B; 1.
KW Hypothetical protein; Hydrolase; Zinc; Complete proteome.
FT METAL 54 54 ZINC 1 (BY SIMILARITY).
FT METAL 56 56 ZINC 1 (BY SIMILARITY).
FT METAL 58 58 ZINC 2 (BY SIMILARITY).
FT METAL 59 59 ZINC 2 (BY SIMILARITY).
FT METAL 130 130 ZINC 1 (BY SIMILARITY).
FT METAL 149 149 ZINC 1 AND 2 (BY SIMILARITY).
FT METAL 190 190 ZINC 2 (BY SIMILARITY).
SQ SEQUENCE 211 AA; 23225 MW; 1EDA9355F9F8E4F0B CRC64;
Query Match 8.1%; Score 107; DB 1; Length 211;
Best Local Similarity 22.2%; Pred. No. 0.051;
Matches 43; Conservative 27; Mismatches 62; Indels 62; Gaps 7;
QY 79 EEDRVNLRKGVPEPELDLYIISHLHFDHAG----- 111
DB 32 EGHKINQVKEKGLTP---LALLTHAFHDHIGALDEVRKWDIPVYLHNEKWLADAS 88
QY 112 --GNGAFINTEPIVQRAEYEAQAQSEYELKECILFNLYKIIIEGDEVVPG---VQLLHT 166
DB 89 LNSGMLRGIEVTAKPADH-----LIEGDGELNIGPFHLETLFT 127
QY 167 PGHTPGHSLIETKSGPVLITDASYTKENFENFVFGFDSLELASSIKRLKEVYMK 226
DB 128 FGHSPGSVSYV---KADLVISGDVLF--QGGIGRTDLIGNQETLITSIH-KLLTLP 181
QY 227 EKPIVFFGHDIQE 240

DB 182 EHTLVLSHGHPETD 195
RESULT 12
YCBL ECOLI STANDARD; PRT; 215 AA.
ID YCBL ECOLI
AC P75849;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ycbL.
GN YCBL OR B0927.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RC MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RC MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa K., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takenoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map."
RL DNA Res. 3:137-155(1996)
CC -!- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY. STRONG, TO
CC H. INFLUENZAE HI1663.
CC
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CC
CC EMBL; AE000195; AAC74013.1; --
CC EMBL; D90730; BAA35673.1; --
CC EMBL; D90731; BAA35679.1; --
CC PIR; F64832; F64832.
CC EcoGene; EG13704; ycbL.
DR InterPro; IPR001279; Blactamase-like.
DR Pfam; PF00753; lactamase B; 1.
KW Hypothetical protein; Hydrolase; Zinc; Complete proteome.
FT METAL 56 56 ZINC 1 (BY SIMILARITY).
FT METAL 58 58 ZINC 1 (BY SIMILARITY).
FT METAL 60 60 ZINC 2 (BY SIMILARITY).
FT METAL 61 61 ZINC 2 (BY SIMILARITY).
FT METAL 132 132 ZINC 1 (BY SIMILARITY).
FT METAL 151 151 ZINC 1 AND 2 (BY SIMILARITY).
FT METAL 192 192 ZINC 2 (BY SIMILARITY).
SQ SEQUENCE 215 AA; 23784 MW; C4233FF08308B18D CRC64;
Query Match 8.1%; Score 106.5; DB 1; Length 215;
Best Local Similarity 26.2%; Pred. No. 0.058;
Matches 53; Conservative 26; Mismatches 48; Indels 75; Gaps 13;


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QY 79 BEDRVNVL-----KRVGYEPD-----LLYIISHLHFDHAGNGAFINTPIIVQRAEY 128
Db 21 EQTRIALALVDPGGDAEKIKQEVDDSGLTMLQILLTHGLDHSV-----AAA 66

QY 129 EAAQH-----SEBY-----LKEC--ILPN--LNYKIIEGDYEVVPGV 161
Db 67 ELAQHYGVVFGPEKEDFWLQGLPAQSRMGLEQCPLTPDRWLN-----EGDIISGNV 122

QY 162 --QLLHTPGHTPGHQSLLIETEK---SGPVLLTTDASYTKENFENVEVFAFG---DSELA 213
Db 123 TLQVLHCFGHTPGHVFWDDRAKLISGDVI-----FKGGVGRSDFPRGRHNQL 171

QY 214 LSSIKRLKEVVMKEKPIVFFGH 235
Db 172 ISSIKD-KLLPLGDDVIFPGH 192

RESULT 13
YND2 YEAST
ID YND2 YEAST STANDARD; PRT; 281 AA.
AC P53965;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 32.8 kDa protein in NCE3-HHT2 intergenic region.
GN YNL032W OR N2746.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Duernhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,
RA Hilbert H., Moestl D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: TO YEAST YNL056W AND YNL099C.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z71308; CAA95895.1; -.
DR PIR; S62954; S62954.
DR SGD; S0004977; SIW14.
DR GO; GO:0006950; P:response to stress; IGI.
DR InterPro; IPR004861; Put_tyr_phos.
DR Pfam; PF03162; Y_phosphatase; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 281 AA; 32755 MW; 88BD8AFC620B4570 CRC64;

Query Match 8.0%; Score 105.5; DB 1; Length 281;
Best Local Similarity 20.2%; Pred. No. 0.1;
Matches 51; Conservative 41; Mismatches 71; Indels 89; Gaps 13;

QY 43 EEPGILVDTPGSPASVANNNEGLNFTFVGQVLPMTBEDRVN-----ILKRV--GYEPED 96
Db 36 EDGKLLIDNG-----DGRDIIHQEDKLLSVFNEVLKRFHGEKSD 78

QY 97 LLYIISHLHFDHAGNGAFINTPIIVQRAEYEAQHSSEYKLECIPLNLYKIIEGDYE 156
Db 79 I-----PRKEFDEDDG-----YDSNEHHQKTIE--VMNLTNHLVI---NKE 115

QY 157 VPGVQLLHTPGHT-----PGHQ--SLLIETKSGPVLLITDASYTKENFE----- 200
Db 116 VIPPENFHVVGELYSRSPFRQENFSLHERLKLKSLVLIPEYPOENLFLKLTGKIL 175

QY 201 -----NEVPFAGFDSSELASSIKRLKEVVMK--EKPIVFFGHDIQERGC----- 243
Db 176 YQVMSGNKPEFVNPISHLTKAL-----EIVLNPANQPIILHCNKGHRTGCLIGCIRKL 231

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QY 244 -----KVFPEY 249
Db 232 QNWSLTWIFDEY 243

RESULT 14
GL2C ARATH
ID GL2C ARATH STANDARD; PRT; 258 AA.
AC O24496; O04844;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hydroxyacylglutathione hydrolase cytoplasmic (EC 3.1.2.6) (Glyoxalase
DE II) (Glx II).
GN GLX2-2 OR AT3G10850 OR T7M13.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Wassilewskija;
RA MEDLINE=98009983; PubMed=9349270;
RA Maiti M.K., Krishnasamy S., Owen H.A., Makaroff C.A.;
RA "Molecular characterization of glyoxalase II from Arabidopsis
RA thaliana.";
RT Plant Mol. Biol. 35:471-481(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Leaf;
RX MEDLINE=97218101; PubMed=9065762;
RA Ridderstroem M., Mannervik B.;
RT "Molecular cloning and characterization of the thiolesterase
RT glyoxalase II from Arabidopsis thaliana.";
RL Biochem. J. 322:449-454(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delsen M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choiane N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E.; Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
RA Reichelt J., Schaefer M., Schoen O., Barges M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., van Aken S.,
RA Pai G., Miltischer J., Sellers F., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Niernan W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asanizu E.,
RA Sasamoto S., Kimura T., Ideawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RA "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RA thaliana.";
RN Nature 408:820-822(2000).
CC -|- FUNCTION: Thiolesterase that catalyzes the hydrolysis of S-D-
CC lactoyl-glutathione to form glutathione and D-lactic acid.
CC -|- CATALYTIC ACTIVITY: (S) - (2-hydroxyacyl)glutathione + H(2)O =

```

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CC glutathione + a 2-hydroxy acid anion.
CC -!- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
CC -!- PATHWAY: Glyoxal pathway.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
CC -----
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CC -----
CC EMBL; Y09029; AAC49867.1; -.
CC DR EMBL; Y08357; CAA69644.1; -.
CC DR EMBL; AC011708; AAF19564.1; -.
CC DR HSSP; Q16775; 1QH5.
CC DR InterPro: IPR001279; Blactmase-like.
CC DR Pfam; PF00753; lactamase_B; 1.
CC KW Hydrolase; Zinc.
CC FT METAL 54 54 ZINC 1 (BY SIMILARITY).
CC FT METAL 56 56 ZINC 1 (BY SIMILARITY).
CC FT METAL 58 58 ZINC 2 (BY SIMILARITY).
CC FT METAL 59 59 ZINC 2 (BY SIMILARITY).
CC FT METAL 112 112 ZINC 1 (BY SIMILARITY).
CC FT METAL 135 135 ZINC 1 AND 2 (BY SIMILARITY).
CC FT METAL 174 174 ZINC 2 (BY SIMILARITY).
CC FT METAL 14 14 S -> T (IN REF. 1).
CC FT CONFLICT 85 93 GCTDAVDNG -> VALMRLIC (IN REF. 1).
CC FT CONFLICT 98 102 LGQDI -> WSGY (IN REF. 1).
CC FT CONFLICT 122 122 N -> T (IN REF. 1).
CC SQ SEQUENCE 258 AA; 28792 MW; 6703B98A8F902B5A CRC64;

Query Match 7.6%; Score 100.5; DB 1; Length 258;
Best Local Similarity 18.4%; Pred. No. 0.24;
Matches 43; Conservative 33; Mismatches 51; Indels 107; Gaps 9;

QY 93 EPEDLL-----YIISHLHFDHAGNGAFINPIVQRAEYAAQHSSEYLKEC 141
DB 32 DPEKVIASAEKHOAKIKFVLTHHHWDHAGN-----EKIKQ- 68
QY 142 ILPLNMYKITEGDEVVPG-----VQLLHTPGHTPGHQSLLIE-TEK 182
DB 69 LVFDI--KVYGGSLDKVKGCTDAVDNGDKLTGLQDINILALHTPCHTKGHISYYVNGKEG 126
QY 183 SGPVLLTIDA-----SYTKENFE----- 200
DB 127 ENPAVFTGDTLFFVAGCGKFEFGTAEQMYQSLCVTLAALPKPTQVYCGHEVTVKNLEFALT 186
QY 201 -----NEVPFAGFDSALSSIKRLKEVVMKEKPIVFFGH-DIEQERGCK 244
DB 187 VEPNNGKIQKLAWARQQOQADLPITPSTILEELETNPPMRVKPEIQEKLCK 240

RESULT 15
YFBB BACSU
ID YFBB BACSU STANDARD; PRT; 220 AA.
AC P37502;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yfbb.
GN YFBB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX Ogasawara N., Nakai S., Yoshikawa H.;
RA MEDLINE=96051385; PubMed=7584024;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus

RT subtilis chromosome containing the replication origin.";
RL DNA Res. 1:1-14(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertsch M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Broutillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Deniot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Etian K.D., Errington J., Fabret C., Ferrar E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinis S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield P.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC -----
CC EMBL; D26185; BAA05201.1; -.
CC DR EMBL; Z99124; CAB16107.1; -.
CC DR PIR; S65995; S65995.
CC DR Subtilist; BG10029; Yybb.
CC DR InterPro: IPR001279; Blactmase-like.
CC DR Pfam; PF00753; lactamase_B; 1.
CC KW Hypothetical protein; Complete proteome.
CC SQ SEQUENCE 220 AA; 25266 MW; 57AF02520BA1A3C5 CRC64;

Query Match 7.6%; Score 99.5; DB 1; Length 220;
Best Local Similarity 23.9%; Pred. No. 0.23;
Matches 43; Conservative 25; Mismatches 63; Indels 49; Gaps 9;

QY 31 LDLPVWCYLLETGEPILVDTGMPESAVNNEGLFNGTFVSGOVLPMKTEEDRVNILKRV 90
DB 21 LRIPVHTWFIKDDGVYIVDTGIER-----FADAQIRALAA-----I 57
QY 91 GYEPEDLLYIISHLHFDHAGNGAFI---NTPIIIVQRAEYAAQHSSEYLKECILPLN 147
DB 58 G-NPKAILL---THGSDHIGGASKWLERDPIFAHOKELKYLNGEPEY-----PNKN 107
QY 148 YKIEGDEVVPGV---QLLH-----TPGHTPGHQSLLIETKSGPVLITDASYTKE 197
DB 108 EVENTGVAHIVQPLTEQTLAHLPLKYLTPCHSPGH---VYVYHKIDRTLLTGDLFITSK 164

Search completed: February 20, 2004, 16:25:12
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Job time : 18 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2004, 16:26:08 ; Search time 34 Seconds
(without alignments)
1539.576 Million cell updates/sec

Title: US-10-019-661-2

Perfect score: 1315

Sequence: 1 MTVKLLYFVAGRCMLDHS.....VFFGHDIQERCKVFPEYI 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 205382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pap.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pap.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pap.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pap.*
12: /cgn2_6/ptodata/1/pubpaa/US09C_NEW_PUB.pap.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pap.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153.5	11.7	290	15	US-10-156-761-8756 Sequence 8756, Ap
2	142.5	10.8	249	15	US-10-156-761-9011 Sequence 9011, Ap
3	130.5	9.9	372	15	US-10-156-761-13378 Sequence 13378, A
4	123.5	9.4	285	12	US-10-264-237-2716 Sequence 2716, Ap
5	120.5	9.2	378	15	US-10-156-761-7704 Sequence 7704, Ap
6	119	9.0	298	9	US-09-925-301-1224 Sequence 1224, Ap
7	109.5	8.3	274	12	US-10-369-493-1669 Sequence 1669, Ap
8	109	8.3	361	12	US-10-216-163-8 Sequence 8, Appli
9	109	8.3	361	12	US-10-218-765-8 Sequence 8, Appli
10	109	8.3	361	12	US-10-219-063-8 Sequence 8, Appli
11	109	8.3	361	12	US-10-219-066-8 Sequence 8, Appli
12	109	8.3	361	12	US-10-219-067-8 Sequence 8, Appli
13	109	8.3	361	12	US-10-219-068-8 Sequence 8, Appli
14	109	8.3	361	12	US-10-219-069-8 Sequence 8, Appli
15	109	8.3	361	12	US-10-219-073-8 Sequence 8, Appli

16	109	8.3	361	12	US-10-219-475-8	Sequence 8, Appli
17	109	8.3	361	12	US-10-219-480-8	Sequence 8, Appli
18	109	8.3	361	12	US-10-219-483-8	Sequence 8, Appli
19	109	8.3	361	12	US-10-219-525-8	Sequence 8, Appli
20	109	8.3	361	12	US-10-219-526-8	Sequence 8, Appli
21	109	8.3	361	12	US-10-219-530-8	Sequence 8, Appli
22	109	8.3	361	12	US-10-219-531-8	Sequence 8, Appli
23	109	8.3	361	12	US-10-219-532-8	Sequence 8, Appli
24	109	8.3	361	12	US-10-219-533-8	Sequence 8, Appli
25	109	8.3	361	12	US-10-230-437-8	Sequence 8, Appli
26	109	8.3	361	12	US-10-232-228-8	Sequence 8, Appli
27	109	8.3	361	12	US-10-232-226-8	Sequence 8, Appli
28	109	8.3	361	12	US-10-230-130-8	Sequence 8, Appli
29	109	8.3	361	15	US-10-227-884-8	Sequence 8, Appli
30	109	8.3	361	15	US-10-230-163-8	Sequence 8, Appli
31	109	8.3	361	15	US-10-230-338-8	Sequence 8, Appli
32	109	8.3	361	15	US-10-218-631-8	Sequence 8, Appli
33	109	8.3	361	15	US-10-230-414-8	Sequence 8, Appli
34	109	8.3	361	15	US-10-216-159A-8	Sequence 8, Appli
35	109	8.3	361	15	US-10-218-849-8	Sequence 8, Appli
36	109	8.3	361	15	US-10-227-873-8	Sequence 8, Appli
37	109	8.3	361	15	US-10-227-883-8	Sequence 8, Appli
38	109	8.3	361	15	US-10-219-076-8	Sequence 8, Appli
39	109	8.3	361	15	US-10-230-434-8	Sequence 8, Appli
40	109	8.3	361	15	US-10-219-003-8	Sequence 8, Appli
41	109	8.3	361	15	US-10-219-075-8	Sequence 8, Appli
42	109	8.3	361	15	US-10-219-464-8	Sequence 8, Appli
43	109	8.3	361	15	US-10-219-466-8	Sequence 8, Appli
44	109	8.3	361	15	US-10-219-479-8	Sequence 8, Appli
45	109	8.3	361	15	US-10-219-481-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-156-761-8756
; Sequence 8756, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8756
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8756

Query Match 11.7%; Score 153.5; DB 15; Length 290;
Best Local Similarity 25.7%; Pred. No. 2.5e-07;

Matches 61; Conservative 44; Mismatches 93; Indels 39; Gaps 11;

Qy 37 CYLLETE-EGPILVDTGMPESAVNNGLFNGTFTVEQVLPKMTTEEDRIVNLKRVGEPE 95

Db 41 CLLVETDRDGLVIVESGIGTADVARPEQNLGADFLGRAQPVLDLAETALHQTGLGFRPE 100

Qy 96 DLLYITSSHLHFHAGNGAFINTPIVQPAEYEAQ-----HSEYLLKE-----CILPN 145

Db 101 GVRHIVLSHLLDHDAGLSDFPWAKVLTAEHRAAAMPAGHPEDKRVRYRPAQWAHRPH 160

Query March	9.4%	Score 123.5	DB 12	Length 285
Best Local Similarity	25.4%	Pred. No. 0.00031		
Matches 60	Conservative 28	Mismatches 71	Indels 77	Gaps 12
QY	39	LLTEEGPILVDTGMPESAVNNEGLFNGTFVGGVQLPKMTEEDRIVNILKKRVGYEPEDLL	98	
Db	76	LEEAARGPILVDTGCPWA	-----	REALGALAGQMGAGDVT 112
QY	99	YIISSHLFPHAGNGGAFINTPIIVQRAYEAAQHSEYLKECILPNLNYKI	-----	TGDD 154
Db	113	LVGTGHGSHDIGNLGFPGNALVSH	-----	DFCLPGGRYLPHGIGERP 158
QY	155	YEVVPGVQLLTGPGHTPHQ	---SLLIETKSGPVLTTIDASYTKENPENEVPFAGTFPSE	211

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (279)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1224

Query Match          9.0%; Score 119; DB 9; Length 298;
Best Local Similarity 24.4%; Pred. No. 0.00096;
Matches 53; Conservative 31; Mismatches 63; Indels 70; Gaps 10;

Qy   38 YLLETEREGPILVDGMPESAVNNEGLEFNGTFVEGVLPKMTEDRIVNILKRVGYPEDL 97
      ||| : ||| ||| | :|| : ||| :
Db   44 YLVGTGPRILIDTGP-----AIPE-----YISCLKALTEFNTA 79

Qy   98 LY-IISHLHFDIAGGNAP---INT-----PIIVORAEYEA-AQHSEFYKCECIL 143
      | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   80 IQEIVVTHWRDHSGGIGDICKSINNDDTYCIIKKLPNPQREEIIGNGEQQOYYVLK---- 135

Qy   144 PNLNYKIIEGDYEVWPG--VOLLIHTPGTGHQSLLJETEK---SGPVLLITIDASYTEKN 198
      : || : || : || : || : || : || : || : || : || : || : || : ||
Db   136 -----DGVINKTEGATUKVLTPGHTDDHMALLEENNAIFSGDCILGEGTVTFEDL 187

Qy   199 FENEVPFAGFDSSELALSIRKLKEVNMKEPVFVFGH 235
      : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : |||
Db   188 YD-----YMSLSKELLKIKADIYPGH 209

RESULT 7
US-10-369-493-1669
; Sequence 1669, Application US/10369493
; Publication No. US20030233675A1
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1. APPLICANT: Cao, Yongwei
 2. APPLICANT: Hinkle, Gregory J.
 3. APPLICANT: Slater, Steven C.
 4. APPLICANT: Goldman, Barry S.
 5. APPLICANT: Chen, Xianfeng
 6. TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
 7. TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 8. FILE REFERENCE: 38-10(52052)B
 9. CURRENT APPLICATION NUMBER: US/10/369,493
 10. CURRENT FILING DATE: 2003-02-28
 11. PRIOR APPLICATION NUMBER: US 60/360,039
 12. PRIOR FILING DATE: 2002-02-21
 13. NUMBER OF SEQ ID NOS: 47374
 14. SEQ ID NO 1669
 15. LENGTH: 274
 16. TYPE: PRT
 17. ORGANISM: *Saccharomyces cerevisiae*
 18. US-10-369-493-1669

[illegible]

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RESULT 8
US-10-216-163-8
; Sequence 8, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C3
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04

; Sequence 8, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C19
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04

Query Match      8.3%; Score 109; DB 12; Length 361;
Best Local Similarity 22.7%; Pred. No. 0.014;
Matches 49; Conservative 33; Mismatches 62; Indels 72; Gaps 10;

QY 63 LFNQVTEGVGVLPKMTEDRIVNLL-----KRVGVEPED-----LLVILS 102
Db 91 LFNQV-----KVLPIVLSNYSYLIIDTQQLAVAVDPSPRAVOASIEKGVTLVAILC 146
QY 103 SHLHFDHAGNGAFINTPIIVQRAEYEAQHSSEYLYKBCI-----LFLNLYKIIEGD 154
Db 147 THKHWDHSGGNRDL-----SRRH-----RDCRVGSPQDGPVLYTHPLCHQD 188
QY 155 YEVPVGVQL--LHTPGHTPGHQSLLIETEK-----SGPVLLITDASVTKENFENVP 204
Db 189 WSVGRLQIRALATPGCTQGHLYLLDGEYPKGCFLFSGDLLFLSGCGRTFEG----- 242
QY 205 FAGDSLSLSSIKRLKEVVMKPIVFFGHGHDIEQ 240
Db 243 ----NAETMLSSLDTV--LGLGDDTLMLPFGHEYAE 272

; SEQ ID NO 8
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-8

Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
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; Publication No. US20030187204A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Smith, William I.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3530P1C31

; CURRENT APPLICATION NUMBER: US/10/219,067

; PRIOR FILING DATE: 2002-08-14

; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/062287

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063549

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/064103

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 60/069873

; PRIOR FILING DATE: 1997-12-17

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 8

; LENGTH: 361

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-219-067-8

Query Match 8.3%; Score 109; DB 12; Length 361;

Best Local Similarity 22.7%; Pred. No. 0.014;

Matches 49; Conservative 33; Mismatches 62; Indels 72; Gaps 10;

Qy 63 LFNCTFVEGVQLPKMTBEDRIVNLT-----KRVGYEPED-----LLYIIS 102

Db 91 LFNQV----KVLPTPLVSDNYSLIIDTQQLAVAVDPSDPRVAVQASIEKEGVTVAIIC 146

Qy 103 SHLHFDHAGNGAFINPTPIVQRAEYEAQHSEYKECI-----LPLNLYKIIEGD 154

Db 147 THKHWDHSGGNRDL-----SRRH-----RDCRVYGSQDGIPIVLTPLCHQD 188

Qy 155 YEVVPGVQL--LHTPGTPOHQSLLIETEK-----SGPVLITIDASYTKENFENEVP 204

Db 189 VVSVGRQLIRALATPGTQGHVLLDGEPEYKGPSCFLSGDGLLFLSGCGRTFEG-- 242

Qy 205 FAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240

Db 243 ----NAETMLSSLDTV--LGLGDDTLLWPGHEYAE 272

RESULT 13

US-10-219-068-8

; Sequence 8, Application US/10219068

; Publication No. US20030187205A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3530P1C31

; CURRENT APPLICATION NUMBER: US/10/219,068

; CURRENT FILING DATE: 2002-08-13

; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/062287

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063549

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/064103

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 60/069873

; PRIOR FILING DATE: 1997-12-17

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 8

; LENGTH: 361

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-219-068-8

Query Match 8.3%; Score 109; DB 12; Length 361;

Best Local Similarity 22.7%; Pred. No. 0.014;

Matches 49; Conservative 33; Mismatches 62; Indels 72; Gaps 10;

Qy 63 LFNCTFVEGVQLPKMTBEDRIVNLT-----KRVGYEPED-----LLYIIS 102

Db 91 LFNQV----KVLPTPLVSDNYSLIIDTQQLAVAVDPSDPRVAVQASIEKEGVTVAIIC 146

Qy 103 SHLHFDHAGNGAFINPTPIVQRAEYEAQHSEYKECI-----LPLNLYKIIEGD 154

Db 147 THKHWDHSGGNRDL-----SRRH-----RDCRVYGSQDGIPIVLTPLCHQD 188

Qy 155 YEVVPGVQL--LHTPGTPOHQSLLIETEK-----SGPVLITIDASYTKENFENEVP 204

Db 189 VVSVGRQLIRALATPGTQGHVLLDGEPEYKGPSCFLSGDGLLFLSGCGRTFEG-- 242

Qy 205 FAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240

Db 243 ----NAETMLSSLDTV--LGLGDDTLLWPGHEYAE 272

RESULT 14

US-10-219-069-8

; Sequence 8, Application US/10219069

; Publication No. US20030187206A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

```

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C40
; CURRENT APPLICATION NUMBER: US/10/219,069
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 8
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-069-8

Query Match      8.3%; Score 109; DB 12; Length 361;
Best Local Similarity 22.7%; Pred. No. 0.014;
Matches 49; Conservative 33; Mismatches 62; Indels 72; Gaps 10;

QY 63 LFNQTFVEGVQLPKMTEEDRIVNLI-----KRVGYEPED-----LXYIIS 102
Db 91 LFNQV-----KVLPIPVLSNYSYLIIDTQQLAVAVDPSDPRVQASIEKEGVTLVAILC 146
QY 103 SHLHFDHAGNGAFINTPIIVQRAEYEAQHSSEYKKECI-----LPLNLYKIIEGD 154
Db 147 THKHWDHSGGNRDL-----SRRH-----RDCRVYGSPOQDGIPLYLTHPLCHQD 188
QY 155 YEVVPGVQL--LHTPGHTPGHQSLLIETEK-----SGVLLTTIDASYTKENFENEVP 204
Db 189 VWSVGRLOIRALATPGHTQGHLYVLDGEPYKGPSCLFSGDLLFLSCGRTFEG-----242
QY 205 FAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
Db 243 ----NAETMLSSLDTV--LGLGDDTLLWPGHEYAAE 272

```

RESULT 15

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US-10-219-073-8
; Sequence 8, Application US/10219073
; Publication No. US20030187207A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

```

```

; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C52
; CURRENT APPLICATION NUMBER: US/10/219,073
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 8
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-073-8

Query Match      8.3%; Score 109; DB 12; Length 361;
Best Local Similarity 22.7%; Pred. No. 0.014;
Matches 49; Conservative 33; Mismatches 62; Indels 72; Gaps 10;

QY 63 LFNQTFVEGVQLPKMTEEDRIVNLI-----KRVGYEPED-----LXYIIS 102
Db 91 LFNQV-----KVLPIPVLSNYSYLIIDTQQLAVAVDPSDPRVQASIEKEGVTLVAILC 146
QY 103 SHLHFDHAGNGAFINTPIIVQRAEYEAQHSSEYKKECI-----LPLNLYKIIEGD 154
Db 147 THKHWDHSGGNRDL-----SRRH-----RDCRVYGSPOQDGIPLYLTHPLCHQD 188
QY 155 YEVVPGVQL--LHTPGHTPGHQSLLIETEK-----SGVLLTTIDASYTKENFENEVP 204
Db 189 VWSVGRLOIRALATPGHTQGHLYVLDGEPYKGPSCLFSGDLLFLSCGRTFEG-----242
QY 205 FAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
Db 243 ----NAETMLSSLDTV--LGLGDDTLLWPGHEYAAE 272

```

Search completed: February 20, 2004, 16:31:37
Job time : 36 secs

111	FFHD-----ADEHTLPAALADAGTAISDIDAVVASHLHLDHAGGRHFAGTDDTPIYVH	169
125	RAEY-----EAAQHSBEYLKECILPMLANKI--EGDYVPGVQQLLHTPGH	169
139	RAEY-----EAAQHSBEYLKECILPMLANKI--EGDYVPGVQQLLHTPGH	169
165	EREGLGYARSAATDTGSIAYHSPDFRA-----LNNRVVAVDGRGRQLPGDLLHLPGH	219
170	TPGHQSLLIETEK--SGPVLTIDASYTKENFENEVFA--GFQSELA--LSSITKRLKEVVM	225
220	TPGLGLGLEPEDGAAPAVGADEAYQRENYEDGVPMATSLSSLDADWESRRRVNDLAK	279
226	KEKPIVFFGHD	236
280	RTTADVFCGH	290

RESULT 4

D69438

hypothetical protein AF1509 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C:Accession: D69438

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkland, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Glöckle, A.; Zhou, L.; Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing bacterium Archaeoglobus fulgidus

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: D69438

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-262 <KLE>

QY	93	EPEDLLYIISHLHFDHAGNGAFINTPIIVORAEVEA-----QHSEEYLKCEILP--N	145
Dd	82	KPEDVDKLIITLHFDHAANAALFTNARIYYQKKEWESALNPPLHYRQTDDSSMLPLEE	141
QY	146	LNKYIEGDYEVVPGVQLLHTPGTTPGHQSLLIETKSGPVLLTIDASYTKENF-----	199
Dd	142	MOLCLIDGVEIAEGVKAVLLPGHTKGLOGVALETEK-GTYLLAAADHFYTFYFFPPKPQ	200
QY	200	-----ENEVPF--AGDFDELALLSKRIUKLEVVMKEKPTVFFGHDIEQERG	243
Dd	201	IQMTDTAGNTVEIPTSPFLFPGLHVLDSEWESCFAKSAKKANILPDGDFSLEG--	258
QY	244	KVPF	247
Dd	259	RVPF	262

C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: D75552
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodd,
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: D75552

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: G75350
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-253 <WHI>
A:Cross-references: GB:AE002022; GB:AE000513; NID:g6459590; PIDN:AAF11372.1; PID:g645959
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1823
A:Map position: 1

Query Match 14.1%; Score 186; DB 2; Length 253;
Best Local Similarity 27.1%; Pred. No. 4e-08;
Matches 49; Conservative 35; Mismatches 63; Indels 34; Gaps 7;
QY 47 ILVDTGMPESAVNNEGLFNGTFVGGQVLPKM---TTEDRIVNLIKRVGVEPEDLLYIIS 103
DB 38 VLIVETGMDRG-----GKFEQMYALERDETFFRGLRDVGVEPDDIDLVINT 84
QY 104 HLHFDHAG-----GNGAFINTPIIVQRAEYEAQAQSEE-----YLKCEILPNLN---YK 149
DB 85 HLHFDHCGRNTGLTGEPTFNARYVVOQVHDLATHTERSRASYIADTFWPIHEAGLFD 144
QY 150 IIEGDYEVVPGVOLLHTPGTGHQSLIETKSGPVLLTIDASYTKENFENEPVFA-GF 208
DB 145 LVDGETELLPLGLVLPGLHNGQGVVL---RSGGQTLVVADVIVPTTAHAPYPYVMGY 201
QY 209 D 209
DB 202 D 202

RESULT 9
G89959
conserved hypothetical protein SA1568 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: G89959
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Qui, L.; Oguc
ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89959
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-280 <KUR>
A:Cross-references: GB:BA000018; PID:g13701542; PIDN:BA842836.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1568

Query Match 14.0%; Score 183.5; DB 2; Length 280;
Best Local Similarity 23.7%; Pred. No. 7.5e-08;
Matches 55; Conservative 48; Mismatches 76; Indels 53; Gaps 8;
QY 31 LDLPVWCYLLETESGPILVDTGMPESAVNNEGLENGTFVGGQVLPKMTEDRIVNLIKRV 90
DB 44 INLPTHPILTAQYLNLIIDAGIENGKLSKQLRNF-----GVDEESHIIADLAN 94
QY 91 GYEPEDLLYIISHLPHDA-----GNGAFINTPIIVQRAEYEAQAQSEEYLKCEILP 144
DB 95 NLTPEKIDYVLMTHGFHDAAGLTDQAGHAIFENAIHVQQDEWH-----EFTAP 144
QY 145 NLNLYK-----IIEGDYEVVPGVOLLHTPGTGHQSLIETKSGPVLL 188
DB 145 NIRSSTYWNKNGDYSNKLILFEKHFEPVPGIKMQHSGHSGFHTIITIESQ--GDKAV 202
QY 189 TIDASYTKENFENEPVFAAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQE 240

DB 203 HMGDIFPTTAHKNPLWVTAYD-DYPMQSIRES-----KERMIPYF---IQQQ 244

RESULT 10
D69036
conserved hypothetical protein MTH1267 - Methanobacterium thermoautotrophicum (strain De
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: D69036
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, N.; Hamlin, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: D69036
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-205 <MTH>
A:Cross-references: GB:AE000893; GB:AE000666; NID:g2622375; PIDN:AA85756.1; PID:g262233
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1267
C:Superfamily: glyoxalase

Query Match 13.1%; Score 172.5; DB 2; Length 205;
Best Local Similarity 26.3%; Pred. No. 4e-07;
Matches 56; Conservative 39; Mismatches 73; Indels 45; Gaps 10;
QY 28 GELLDLPLVWCYLLETESGPILVDTGMPESAVNNEGLENGTFVGGQVLPKMTEDRIVN 87
DB 13 GTLFDSNM--YIL---GDTIVDTG---TGMN-----PDALLARM 43
QY 88 KRVGYEPEDLLYIISHLPHDAGNGAFINTPIIVQRAEYEAQAQSEE-----YLKECI 142
DB 44 RGAGVNPSDIKHIVNTHCHFDHTGGRNLF--DADIAHSLDADALREGDARTVAYMFSA 102
QY 143 LPNLYNKIIEGDYEVVPGVOLLHTPGTGHQSLIETKSGPVLLTIDASYTKENFENE 202
DB 103 MDAMDVAVELGEGDFVGDFEVIHTPGTTPGICILY-----EGSLSISGDIVFADGGF-GR 156
QY 203 VPFAGFDSSELALSSIKRLKEVVMKEKPIVFFGH 235
DB 157 VDVGDISELALSSIKRLKEVVMKEKPIVFFGH 185

RESULT 11
H70733
hypothetical protein Rv2300c - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: H70733
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: H70733
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-310 <COL>
A:Cross-references: GB:Z77163; GB:AL123456; NID:g3261610; PIDN:CAB00971.1; PID:e255162;
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: Rv2300c

Query Match 11.9%; Score 157; DB 2; Length 310;
Best Local Similarity 25.7%; Pred. No. 1.4e-05;
Matches 62; Conservative 34; Mismatches 87; Indels 58; Gaps 11;

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Qy      39 LLETEEGPILYDTGM-----PESAVNNEGFLNGFTVEGQVLPKMTEEDRIVNILKRVG 91
Db      74 LVETDDGLVLDVTGTGFIQDCIDLP---GRVGLFRHV---LRPAFLQAETAARQTQLG 124
Qy      92 YEPEDLIIISHLHFDHAGNGAFINTPII VORAEYEAAQHSEEVLYKECLPNLNY--- 148
Db     125 YRTSDVRHIVLTDFDHDIGGIADPEAHLHVTAAEAARGAIHAPS-LRL- ---RYRYRRG 179
Qy     149 -----KLIEGDYEVVP-----GVOLLHTPGHTPGHQSLLIIFETKSGPYL 187
Db     180 QWAHGPKLVEHPDGDPGEWRGFASAKPLDSIGTGVVLVPMFGPTRGHAAVAVDAGHRW-VL 238
Qy     188 LTIDASVTKENFEN--EYPEAGFDSSELALS-----SIKELKEVVMKEKP--IVFFGH 235
Db     239 HCGDAFYHRTGLDGRFVFVFWRAEEKLLSYNNRNQLRONQARIVEIHRHRHDPDLIVCAH 298
Qy     236 D 236
Db     299 D 299

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RESULT 12
AH2652
metallo-beta-lactamase superfamily protein [imported] - Agrobacterium tumefaciens (strain
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C/Accession: AH2652
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.;
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayin, T.; Levy, R.; Li, M.; McClell,
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2311-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AH2652
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333 <KOR>
A/Cross-references: GB:AE008688; PID:AA141638.1; PID:gl7738978; GSPDB:GN00186
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: Atu0622
A/Map position: circular chromosome

RESULT 13
E97434
hypothetical protein AGR_C1105 [imported] - Agrobacterium tumefaciens (strain C58, Cere

C:Species: *Agrobacterium tumefaciens*
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: E97434
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouello, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: E97434
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-370 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK96430.1; PID:gl5155568; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_1105
A:Map position: circular chromosome

RESULT 14
D84057
hypothetical protein BH3260 [imported] - Bacillus halodurans (strain C-125)
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C/Accession: D84057
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirano
C/Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: D84057
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-284 <STO>
A/Cross-references: GB:AF001518; GB:BA000004; NID:G10175792; PIDN:BA06979.1; GSPDB:GN003
A/Experimental source: strain C-125
C/Genetics:
A/Gene: BH3260

	Query Match	11.9%;	Score 156;	DB 2;	Length 284;		
	Best Local Similarity	25.9%;	Pred. No. 1.5e-05;				
	Matches	43;	Conservative	39;	Mismatches	46;	
				Indels	38;	Gaps	7;
<hr/>							
QY	38	YLLETEGPILVDTGPESAVNNEGLNGFTVFGQVL P-KMTEEDRIVNILKRVGYEPD	96				
	:	:::	:	:	:	:	:
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
Dd	54	FLIQDCQNILVES-----GIGNREFTDKRKNYGISESFLEDQLSLGTVA D	103				
<hr/>							
QY	97	LLVIISSHLHFDHAGG-----NGAFINTPIIVQRAEYEAAOHSEYLYKECIIPLNL	146				
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
Dd	104	IDAVLMTHLFDRASGLAKQEGEWST---FENAVIYASAREWAEMRE---PNIRSRNT	157				
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:


```

; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 506
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5506

Query Match      10.1%; Score 132.5; DB 4; Length 326;
Best Local Similarity 23.2%; Pred. No. 8.1e-06;
Matches 62; Conservative 44; Mismatches 100; Indels 61; Gaps 13;

QY 21 VNSTLAPGELLDPVWCYLLTEBEGPILVDTGMPESAVNNEGL---FNGTFV-EGQVYL-- 74
Db 47 ITSLLDGTIYLDPKLKNLSPAKTKILT---KYAAVNEKGIGTQSVNAFLVDDGKSLTL 102
QY 75 -----PKWTEEDRIWNILKRVGYEPEDLLYIISHLHFDHA-----GNGAFINT 119
Db 103 VDSGAASCFCGPQL---GSIAKNLELAGYQLANVKTIVLLTHLPDHVCGIAQNGKAVFPNA 159
QY 120 PIIVQRAEYE-----AAQHSSEYL-----KECILPNLNYKIIIE--GDYEVVPG 160
Db 160 TIYAHERRADYWLNPANEKTVPADKKENYILGTWKNVKAALAPYQAKKAPKTFKDGDIQ 219
QY 161 VQLLHTPGHTPGHQSLIETKSGPVLITIDASYTKENFENFVPGFD---SETALSS 216
Db 220 FEVINTQHTPGHSHFLKSK--GQIVFVCGDIVHSHLSLOFDAPKTCGVDFVNSEQAINT 277
QY 217 -IKRLKEVVMKEK-----PIVFFGH 235
Db 278 RLKMFABISNKQWVAAPHLPPFGIGH 304

RESULT 3
US-09-252-991A-24102
; Sequence 24102, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24102
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24102

Query Match      9.7%; Score 128; DB 4; Length 722;
Best Local Similarity 24.1%; Pred. No. 8.2e-05;
Matches 67; Conservative 29; Mismatches 72; Indels 110; Gaps 13;

QY 7 YFVPAGRCMLDHSVNSTLTTFGELLDPVWCYLLTEBEGPILVDTGMPESAVNNEGLFNG 66
Db 506 YVRPFYRCNMWH-----VQGERDVLVDG-----SG 532
QY 67 TFVEGQVLPKMTEDRIWNILKRVGYEPEDLLYIISHLHFDHAGNGAFINTPIIVQRA 126
Db 533 LVSLREQLPWITERP-----LLAVASTHFDHAGHFEAERLAHPAEA 576
QY 127 EYEAQHSSEYL-----KECILPNLNYK-----IIGDVEVVPG--VQ 162
Db 577 EILAAPDGDNTLARAYVGDEMFEAHPECPLCAEYRVRAAPATRLIDEGDVLIDGRLVQ 636

; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 506
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5506

Query Match      10.1%; Score 132.5; DB 4; Length 326;
Best Local Similarity 23.2%; Pred. No. 8.1e-06;
Matches 62; Conservative 44; Mismatches 100; Indels 61; Gaps 13;

QY 21 VNSTLAPGELLDPVWCYLLTEBEGPILVDTGMPESAVNNEGL---FNGTFV-EGQVYL-- 74
Db 47 ITSLLDGTIYLDPKLKNLSPAKTKILT---KYAAVNEKGIGTQSVNAFLVDDGKSLTL 102
QY 75 -----PKWTEEDRIWNILKRVGYEPEDLLYIISHLHFDHA-----GNGAFINT 119
Db 103 VDSGAASCFCGPQL---GSIAKNLELAGYQLANVKTIVLLTHLPDHVCGIAQNGKAVFPNA 159
QY 120 PIIVQRAEYE-----AAQHSSEYL-----KECILPNLNYKIIIE--GDYEVVPG 160
Db 160 TIYAHERRADYWLNPANEKTVPADKKENYILGTWKNVKAALAPYQAKKAPKTFKDGDIQ 219
QY 161 VQLLHTPGHTPGHQSLIETKSGPVLITIDASYTKENFENFVPGFD---SETALSS 216
Db 220 FEVINTQHTPGHSHFLKSK--GQIVFVCGDIVHSHLSLOFDAPKTCGVDFVNSEQAINT 277
QY 217 -IKRLKEVVMKEK-----PIVFFGH 235
Db 278 RLKMFABISNKQWVAAPHLPPFGIGH 304

RESULT 3
US-09-252-991A-24102
; Sequence 24102, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24102
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24102

Query Match      9.7%; Score 128; DB 4; Length 722;
Best Local Similarity 24.1%; Pred. No. 8.2e-05;
Matches 67; Conservative 29; Mismatches 72; Indels 110; Gaps 13;

QY 7 YFVPAGRCMLDHSVNSTLTTFGELLDPVWCYLLTEBEGPILVDTGMPESAVNNEGLFNG 66
Db 506 YVRPFYRCNMWH-----VQGERDVLVDG-----SG 532
QY 67 TFVEGQVLPKMTEDRIWNILKRVGYEPEDLLYIISHLHFDHAGNGAFINTPIIVQRA 126
Db 533 LVSLREQLPWITERP-----LLAVASTHFDHAGHFEAERLAHPAEA 576
QY 127 EYEAQHSSEYL-----KECILPNLNYK-----IIGDVEVVPG--VQ 162
Db 577 EILAAPDGDNTLARAYVGDEMFEAHPECPLCAEYRVRAAPATRLIDEGDVLIDGRLVQ 636

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20572
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20572

Query Match      8.9%; Score 117.5; DB 4; Length 295;
Best Local Similarity 23.3%; Pred. No. 0.00028;
Matches 60; Conservative 38; Mismatches 90; Indels 69; Gaps 11;

QY 31 LDLPVWCYLLTEBEGPILVDTGMPESAVNNEGLFNGTFVEGQVLPKM--TEEDR--IVNIL 87
Db 47 IDLCRALLVRDGERNVLTETGI-----GAFFPPALRQRYGVQBERHVLDSL 94
QY 88 KRVGYEPEDLLYIISHLHFDHAGNGCA-----FINTPIIVQRAEYEAQHSEE 136
Db 95 AAVGLDDADIDVWLLTHLHFDHAGLLAAWEEGQPARLLFPNAHFVSGRRHWQARQPHP 154
QY 137 YLKECILPN--INXYKIISDYEVW-----PGVOLLHTPGHTPGHQSLIETKSGP 185
Db 155 RDRASFVPELDDLLQASGRLELDDGERSAHLGEGWRFHSEGHTPG--QMLPEIAMPDGP 213
QY 186 VLLTIDASYTKENFENFVPEFA-----GFD--SELALSSIKRLKEVVMKEKPIVFFG 234
Db 214 VVFSGDL-----IPGAPVHPLTWGYDRFPPEGLIEKERLLDLSIARNGLVFT 263
QY 235 HD-----TRQER 241
Db 264 HDPVCAMGRVRRDEQER 280

RESULT 5
US-09-107-532A-5174
; Sequence 5174, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 7310
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Denek
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5174:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...239
; SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

```

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Query Match      8.7%; Score 114.5; DB 4; Length 239;
Best Local Similarity 21.4%; Pred. No. 0.00042;
Matches 62; Conservative 43; Mismatches 80; Indels 105; Gaps 15;

QY 4 KKLFFVPGRC--MLDSSVN-----STLPGELLDLPVWCYLLETEEGPILVDTG 52
DB 5 KLFLEPSNECVILMDERSFGQGMHIERLKTGMIEEN---CYLVYNEALLIIDPG 61
QY 53 MPESAVNNEGLFNGTFVEGVLPKMTEDRIWNILKRVGYEPEDLLYIISSHLHFDHAGG 112
DB 62 -----EADRIKQEIKNQOP-----VAILLTHYDHIGA 93
QY 113 ---NGAFINTP-----IIQVRAEYRAAQHSEEVYKE 140
DB 94 VEPLRAYQIPVYVSPLEQKWLGPILNLSGLGRHDDIADVIVSPAHEFE-----MKT 147
QY 141 CILPLNLYKIEGYEVVPGVQLLHTPGHTGHSQSLIETEKSGPVLITDASYTKENFE 200
DB 148 YTLGNMGR-----VVP-----TPGHSIGSVSFID-----DFVVGDLPRGSIGR 189
QY 201 NEVPEAGDSFELASSIKRLKEVVMKEKPIVFFGH-----DIEQERGCKVP 246
DB 190 TDL--ITG-NLEQLLHSI-RQLFLVLPDEFVAYPGHGDATTIEQEKRTNPF 236

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RESULT 6
US-09-134-001C-3637
; Sequence 3637, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08

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; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3637
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3637

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Query Match      8.1%; Score 106; DB 4; Length 209;
Best Local Similarity 25.0%; Pred. No. 0.0028;
Matches 42; Conservative 26; Mismatches 56; Indels 44; Gaps 9;

QY 23 STLPGELLDLPVWCYLLETEEGPILVDTGMPESAVNNEGLFNGTFVEGVLPKMTEDR 82
DB 6 SNLTG-IVDTNT--YFIENEENVILID---PSS-----ESQK 37
QY 83 IWNILKRVGYEPEDLLYIISSHLHFDHAGNGAFI---NTPIIVQRYE-----AA 131
DB 38 IIKKLNQIN--KPLKAILLTHAHYDHIGALDNIETKYQVFPVYMSKDFDLTDPDKNGS 94
QY 132 QHSEYILKECILPNLN-YKIEGDEVVVP-GVQLLHTPGHTPGHQSLL 177
DB 95 SKFTQYGLSKIESHANPLSLSEGAETEGFKVKVLTHTPGHSPGSLSFV 142

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RESULT 7
US-09-252-991A-18490
; Sequence 18490, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18490
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18490

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Query Match      7.7%; Score 101; DB 4; Length 290;
Best Local Similarity 20.7%; Pred. No. 0.016;
Matches 57; Conservative 37; Mismatches 106; Indels 76; Gaps 12;

QY 13 RCLMDHSSVNSTLTPGELLDLPVWCYLLETEEGPILVDTCMPESAVNNEGLFNG----- 66
DB 52 RVLSSHFAV-----LIEHHAATLLFDTLGLRDI---DAQFRADMPWMA 91
QY 67 --TFVEGVLPKMTEDRIWNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTPIIVQ 124
DB 92 APLFAYQKVVPARDQLDAAGIRVDR-----ILLSHAHWDHAGS---LVDFPEVPV 138
QY 125 RAEEYAAQHSSEYILKECILPN-----LNYKI-----IEGDYEVVPGVQL 163
DB 139 WAPYEETAFSRIATPPAAPPSPQFRHGVRWRPYPSPRPFMGDFDESLLDFGDRLV---L 194
QY 164 LHPTPGHTPGHQSLLIETEKSGPVLITDASYTKENFE--NEVPFAG-----FDSELAISS 216
DB 195 VPLPGHTPGSVGLFVLDSGRRLFFSGDTSWRLEGVGEGPQKFFAGRALVDRDPARTLAQ 254
QY 217 IKELKEVVMKEK--IVFFGHGDIQEERGCKVKVFPEYI 250
DB 255 LAKIR-LLLRSDRLSLVIPAHDARVQAALGYFFPHWL 289

```

RESULT 8
US-08-121-713D-62
; Sequence 62, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 724 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-835-268-62

Query Match 6.9%; Score 90.5; DB 1; Length 724;
Best Local Similarity 22.2%; Pred. No. 0.83;
Matches 54; Conservative 39; Mismatches 87; Indels 63; Gaps 15;

QY 61 EGLFNGTFVEGQ-----VLPKMTEDRIVNILKRVGYEPEDLLYIISHLHFD----- 108
DB 366 QAAFNKGFKEQSSNSAWLPVLSNRVPEPRPGTCVNDTSNLPDVTLVNFIIRSHPLMDKAVN 425
QY 109 HAGNGAF-----INTPIIVORAEYEAQAHSSEYLYKCEILPNLN--YKIIIE-----GD--- 154
DB 426 HEHNPNVYKRDVFTKLVDKIRIDL--NQEIYIVYVGNLGRYIKYIVQYRNGESLS 483
QY 155 -----YEVVP--GVQLLHTPGHTPGHQSLLIETKSGPVLLTIDASYTKNFEN-----E 202
DB 484 KLLDIFEVAPNEAQVMEI---SQRKSLYIGTDHR---IKQIDLAMCNRNRYDNCRCVR 537
QY 203 VPFAGFDSLEALS---SIKRLKEV-----VMKEKPIVFFGHDIIEGRGCKV--FP 247
DB 538 DPYCGWDKEATCRPYELDLQDVANETSDICDSSVLKKIIVVYQGSV--HLGCFVKIP 595
QY 248 EYI 250
DB 596 EVL 598

RESULT 10
US-09-060-692-62
; Sequence 62, Application US/09060692
; Patent No. 5935865
; GENERAL INFORMATION:

US-08-121-713D-62
; Sequence 62, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 724 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-121-713D-62

Query Match 6.9%; Score 90.5; DB 1; Length 724;
Best Local Similarity 22.2%; Pred. No. 0.83;
Matches 54; Conservative 39; Mismatches 87; Indels 63; Gaps 15;

QY 61 EGLFNGTFVEGQ-----VLPKMTEDRIVNILKRVGYEPEDLLYIISHLHFD----- 108
DB 366 QAAFNKGFKEQSSNSAWLPVLSNRVPEPRPGTCVNDTSNLPDVTLVNFIIRSHPLMDKAVN 425
QY 109 HAGNGAF-----INTPIIVORAEYEAQAHSSEYLYKCEILPNLN--YKIIIE-----GD--- 154
DB 426 HEHNPNVYKRDVFTKLVDKIRIDL--NQEIYIVYVGNLGRYIKYIVQYRNGESLS 483
QY 155 -----YEVVP--GVQLLHTPGHTPGHQSLLIETKSGPVLLTIDASYTKNFEN-----E 202
DB 484 KLLDIFEVAPNEAQVMEI---SQRKSLYIGTDHR---IKQIDLAMCNRNRYDNCRCVR 537
QY 203 VPFAGFDSLEALS---SIKRLKEV-----VMKEKPIVFFGHDIIEGRGCKV--FP 247
DB 538 DPYCGWDKEATCRPYELDLQDVANETSDICDSSVLKKIIVVYQGSV--HLGCFVKIP 595
QY 248 EYI 250
DB 596 EVL 598

RESULT 9
US-08-835-268-62
; Sequence 62, Application US/08835268
; Patent No. 5807826

APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,692
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-060-692-62

Query Match 6.9%; Score 90.5; DB 2; Length 724;
Best Local Similarity 22.2%; Pred. No. 0.83;
Matches 54; Conservative 39; Mismatches 87; Indels 63; Gaps 15;
Qy 61 EGLFNGTFVSEQ-----VLPKMTEDRIVNILKRVGYEPEDLLYIISSHLHFD--- 108
Db 366 QAAFNGKFKQSSNSAWLPVLSRVPEPRPGTCVNDTSNLPDTVLNFIIRSHPLMDKAVN 425
Qy 109 HAGNGAF-----INTPIIVQAEYEAQAQSEYKCEILPNLN--YKIIIE-----GD--- 154
Db 426 HEHNNPVYKRDVFTKLVDKIRIDIL--NQEYIVYVVGTLGRIYKIVQYRNGESLS 483
Qy 155 -----YEWVP--GVQLLHTPGTHGOSLLIETKSGPVLLTIDASYTKENFEN-----E 202
Db 484 KLIDIFVAPNEALQWMEI-----SOTRKSLYIGTDHR---IKQIDLAMCNRYYDNCRCVR 537
Qy 203 VPFAGFDSSELALS---SFKRLKEY-----VMKEKPIVFFGHDIQEGERCKV-FP 247
Db 538 DPYCGMDKEATCRPYELDLLQDVANETSDICDSSVLKKKIVVYTGQSV--HLGCFVKIP 595
Qy 248 EYI 250
Db 596 EVL 598

RESULT 11

US-08-833-391-62
Sequence 62, Application US/08833391
Patent No. 6013781
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.

APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,391
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-391-62

Query Match 6.9%; Score 90.5; DB 3; Length 724;
Best Local Similarity 22.2%; Pred. No. 0.83;
Matches 54; Conservative 39; Mismatches 87; Indels 63; Gaps 15;
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Db 366 QAAFNGKFKQSSNSAWLPVLSRVPEPRPGTCVNDTSNLPDTVLNFIIRSHPLMDKAVN 425
Qy 109 HAGNGAF-----INTPIIVQAEYEAQAQSEYKCEILPNLN--YKIIIE-----GD--- 154
Db 426 HEHNNPVYKRDVFTKLVDKIRIDIL--NQEYIVYVVGTLGRIYKIVQYRNGESLS 483
Qy 155 -----YEWVP--GVQLLHTPGTHGOSLLIETKSGPVLLTIDASYTKENFEN-----E 202
Db 484 KLIDIFVAPNEALQWMEI-----SOTRKSLYIGTDHR---IKQIDLAMCNRYYDNCRCVR 537
Qy 203 VPFAGFDSSELALS---SFKRLKEY-----VMKEKPIVFFGHDIQEGERCKV-FP 247
Db 538 DPYCGMDKEATCRPYELDLLQDVANETSDICDSSVLKKKIVVYTGQSV--HLGCFVKIP 595
Qy 248 EYI 250
Db 596 EVL 598

RESULT 12

US-09-060-610-62
Sequence 62, Application US/09060610
Patent No. 6344544
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.

APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,610
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/835,268
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-10151A-62

Query Match 6.9%; Score 90.5; DB 4; Length 724;
Best Local Similarity 22.2%; Pred. No. 0.83;
Matches 54; Conservative 39; Mismatches 87; Indels 63; Gaps 15;
QY 61 EGLFNGTFVEGQ-----VLPKMTEDRIVNLRKVGVEPEDLLYIISSHLHFD---- 108
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DB 426 HEHNNPVYKRDIVFTKLVDKIRIDIL--NQEYIVYVGTNLGRIVKIQQYVYNGESLS 483
QY 155 -----YEVVP--GVQLLHTPGHTPGHOSLLIETKSGPVLTTIDASYTKENFEN-----E 202
DB 484 KLDDIEVAPNEAIQWMEI---SQTRKSLVIGTDHR---IKQIDLAMCNRRYDNCRCVR 537
QY 203 VPFGDFSELALS---SIKELKEV-----VMKEKPIVFFGHDIQEGRGCKV-FP 247
DB 538 DPYCGMDKEANTCRPYELDLQDVANETSDICDSSVLKKKIVVTYQGSV--HLGCFVKIP 595
QY 248 EYI 250
DB 596 EVL 598

RESULT 13
PCT-US94-10151A-62
Sequence 62, Application PC/TUS9410151A
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR HOBBACH TEST ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10151A
FILING DATE: 13-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-10151A-62
Query Match 6.9%; Score 90.5; DB 5; Length 724;
Best Local Similarity 22.2%; Pred. No. 0.83;
Matches 54; Conservative 39; Mismatches 87; Indels 63; Gaps 15;
QY 61 EGLFNGTFVEGQ-----VLPKMTEDRIVNLRKVGVEPEDLLYIISSHLHFD---- 108
DB 366 QAAFNGKFKQSSNSAWLPVLSRVPEPRPGTCVNDTSNLPDTVLNFIKSHPLMDKAVN 425
QY 109 HAGNGAF-----INTPIVORAEYAAQHSSEYKLCILPNLN--YKITE---GD--- 154
DB 426 HEHNNPVYKRDIVFTKLVDKIRIDIL--NQEYIVYVGTNLGRIVKIQQYVYNGESLS 483
QY 155 -----YEVVP--GVQLLHTPGHTPGHOSLLIETKSGPVLTTIDASYTKENFEN-----E 202
DB 484 KLDDIEVAPNEAIQWMEI---SQTRKSLVIGTDHR---IKQIDLAMCNRRYDNCRCVR 537
QY 203 VPFGDFSELALS---SIKELKEV-----VMKEKPIVFFGHDIQEGRGCKV-FP 247
DB 538 DPYCGMDKEANTCRPYELDLQDVANETSDICDSSVLKKKIVVTYQGSV--HLGCFVKIP 595
QY 248 EYI 250
DB 596 EVL 598
RESULT 14
US-08-738-944-50
Sequence 50, Application US/08738944
Patent No. 5783431
GENERAL INFORMATION:
APPLICANT: Peterson, et al.
TITLE OF INVENTION: METHODS FOR GENERATING AND
SCREENING NOVEL METABOLIC PATHWAYS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:

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OM protein - protein search, using sw model

Run on: February 20, 2004, 16:18:56 ; Search time 41 Seconds
(without alignments)
967.845 Million cell updates/sec

Title: US-10-019-661-2

Perfect score: 1315

Sequence: 1 MTVKLLFVPAGRCMLDHS.....VFFGHDIQERCKVFPEYI 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1315	100.0	250	22 AAB50476	Listeria sp. stral
2	1304	99.2	248	23 AAU78814	Bacillus sp. Autoi
3	1244	94.6	250	23 AAU78808	Autoinducer inacti
4	1228	93.4	250	23 AAU78807	Autoinducer inacti
5	1219	92.7	250	23 AAU78804	Autoinducer inacti
6	1213	92.2	250	23 AAU78806	Autoinducer inacti
7	1212	92.2	250	23 AAU78809	Autoinducer inacti
8	1212	92.2	250	23 AAU78811	Autoinducer inacti
9	1209	91.9	250	23 AAU78810	Autoinducer inacti

10	1202	91.4	250	23 AAU78805	Autoinducer inacti
11	1200	91.3	250	23 AAU78812	Autoinducer inacti
12	311	23.7	263	23 AAU78815	Autoinducer inacti
13	145.5	11.1	283	23 ABA48771	Listeria monocytog
14	141	10.7	222	22 AAB96283	Putative P. abyss
15	135.5	10.3	281	22 AAB73541	Burkholderia cepac
16	135.5	10.3	285	21 AAG30597	Arabidopsis thalia
17	135.5	10.3	324	21 AAG30596	Arabidopsis thalia
18	133	10.1	204	22 AAB96055	Putative P. abyss
19	123.5	9.4	285	23 ABB90340	Human polypeptide
20	119.5	9.1	238	23 ABB49158	Listeria monocytog
21	119	9.0	288	22 AAB67569	Amino acid sequenc
22	119	9.0	298	20 AAY73880	Human prostate tum
23	119	9.0	298	21 AAB43779	Human cancer assoc
24	119	9.0	298	22 AAM23487	Novel human enzyme
25	119	9.0	298	22 AAM25792	Human protein sequ
26	118.5	9.0	323	23 ABP51438	Human MDP1 SEQ ID
27	117.5	8.9	331	21 AAG10298	Arabidopsis thalia
28	117	8.9	288	21 AAG10299	Arabidopsis thalia
29	115	8.7	220	21 AAG10300	Arabidopsis thalia
30	114.5	8.7	281	21 AAG41447	Arabidopsis thalia
31	114.5	8.7	286	21 AAG41446	Arabidopsis thalia
32	114.5	8.7	331	21 AAG41445	Arabidopsis thalia
33	113.5	8.6	252	21 AAG31661	Arabidopsis thalia
34	112	8.5	210	23 ABB31851	Arabidopsis thalia
35	109	8.3	361	21 AAY71110	Lactococcus lactis
36	109	8.3	361	23 AAU83595	Human Hydrolase pr
37	109	8.3	385	22 AAM78721	Human PRO protein,
38	108	8.2	228	22 ABB64252	Human protein SEQ
39	106	8.1	209	23 ABP38792	Drosophila melanog
40	105	8.0	271	22 ABB67381	Staphylococcus epi
41	105	8.0	305	22 ABB71300	Drosophila melanog
42	102.5	7.8	282	23 ABU65074	Human NOV17d prote
43	101.5	7.7	258	21 AAG10987	Arabidopsis thalia
44	101.5	7.7	268	21 AAG10986	Arabidopsis thalia
45	101.5	7.7	282	23 ABU65072	Human NOV17b prote

ALIGNMENTS

RESULT 1
ID AAB50476 standard; Protein; 250 AA.
XX AAB50476;
XX AC
XX DT 10-APR-2001 (first entry)
XX DE Listeria sp. strain 240B1 AiiA.
XX KW Listeria; AiiA; autoinducer inactivation protein A; antibacterial;
XX disease resistance; soft rot disease resistance; bacterial infection.
XX OS Listeria sp.
XX PN WO200102578-A1.
XX PD 11-JAN-2001.
XX PF 17-NOV-1999; 99WO-SG00128.
XX PR 02-JUL-1999; 99SG-0003146.
XX (MOLE-) INST MOLECULAR AGROBIOLOGY 1 RES LINK.
XX PA Lian-Hui Z, Yihu D, Jinling X;
XX WPI; 2001-138146/14.
XX N-PSDB; AAF29642.
XX PT New bacterial autoinducer inactivation proteins and nucleic acids
PT encoding the protein, for increasing disease resistance, preventing or

PT reducing bacterial damage to a plant or animal, or treating bacterial
PT infections in animals -
PS Claim 6; Fig 4B; 49pp; English.
XX The present sequence is a bacterial autoinducer inactivation protein
CC (AiiA). It is useful for increasing disease resistance as well as
CC preventing or reducing bacterial damage to a plant or animal. The nucleic
CC acid encoding the AiiA protein may be used to confer resistance to
CC diseases where expression of pathogenic genes are regulated by
CC autoinducers, such as diseases caused by *Pseudomonas aeruginosa*, *Erwinia*
CC *stewartii*, *Xenorhabdus nematophilus*, *Erwinia chrysanthemi*, *Pseudomonas*
CC *solanacearum* and *Xanthomonas campestris*. It may also be used to confer
CC soft rot disease resistance in susceptible plants such as potato,
CC eggplant, Chinese cabbage, carrot and celery. The bacterial autoinducer
CC inactivation protein may be directly used to treat or prevent bacterial
CC infections in animals including humans.

XX Sequence 250 AA;
SQ
Query Match 100.0%; Score 1315; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.6e-134;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTWKLYFVAGRCMLDHSVNSTLTPEGLDLPVWCYLLTEEGPILVDTGMPESAVNN 60
QY 61 EGLFNGTFFVGGQVLPKMTEDRIVNLRKVGYPEDELLYIISSHLHFDHAGNGAFINTP 120
DB 61 EGLFNGTFFVGGQVLPKMTEDRIVNLRKVGYPEDELLYIISSHLHFDHAGNGAFINTP 120
QY 121 IIVQRAEYEAQHSEYLYKECILPNLNKYIEGDIYEVVPGVQLLHTPGHTPGHOSLLIET 180
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DB 181 EKSGPVLLTTDASVTKENFENEPFAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
QY 241 RGCKVFPEYI 250
DB 241 RGCKVFPEYI 250

RESULT 2
AAU78814
ID AAU78814 standard; Protein; 248 AA.

XX AC AAU78814;
XX 18-JUN-2002 (first entry)
XX DE *Bacillus* sp. Autoinducer inactivation protein, AiiA.
XX Autoinducer inactivation; AiiA; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; *Erwinia carotovora*.
XX OS *Bacillus* sp. 240B1.

XX FN WO200216623-Al.
XX 28-FEB-2002.
XX PD 23-AUG-2000; 2000WO-SG00123.
XX PF 23-AUG-2000; 2000WO-SG00123.
XX XX 23-AUG-2000; 2000WO-SG00123.
XX PR (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX PA Zhang L, Dong Y, Xu J;
XX PI Zhang L, Dong Y, Xu J;

DR WPI; 2002-304123/34.

XX Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to
PT a disease in sustainable plant or animal and for reducing bacterial
PT damage -
XX Example 2; Fig 6; 82pp; English.

XX The invention describes an isolated polynucleotide encoding an
CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably
CC human; and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This is the amino acid sequence of the *Bacillus* sp. 240B1 autoinducer
CC inactivation protein AiiA, a putative metallohydrolase and autoinducer
CC inactivation protein.

XX Sequence 248 AA;

Query Match 99.2%; Score 1304; DB 23; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 EGLFNGTFFVGGQVLPKMTEDRIVNLRKVGYPEDELLYIISSHLHFDHAGNGAFINTP 120
QY 121 IIVQRAEYEAQHSEYLYKECILPNLNKYIEGDIYEVVPGVQLLHTPGHTPGHOSLLIET 180
DB 121 IIVQRAEYEAQHSEYLYKECILPNLNKYIEGDIYEVVPGVQLLHTPGHTPGHOSLLIET 180
QY 181 EKSGPVLLTTDASVTKENFENEPFAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
DB 181 EKSGPVLLTTDASVTKENFENEPFAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
QY 241 RGCKVFPE 248
DB 241 RGCKVFPE 248

RESULT 3
AAU78808
ID AAU78808 standard; Protein; 250 AA.

XX AC AAU78808;
XX 18-JUN-2002 (first entry)
XX DE Autoinducer inactivation protein AiiG.
XX Autoinducer inactivation; AiiG; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; *Erwinia carotovora*.
XX OS *Bacillus thuringiensis* B18.

XX FN WO200216623-Al.
XX 28-FEB-2002.
XX PD 28-FEB-2002.

PF 23-AUG-2000; 2000WO-SG00123.
XX
PR 23-AUG-2000; 2000WO-SG00123.
XX
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
PA
PI Zhang L, Dong Y, Xu J;
XX
XX WPI; 2002-304123/34.
DR N-PSDB; ABK47472.
XX
XX Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to
PT a disease in sustainable plant or animal and for reducing bacterial
PT damage -
XX
XX Claim 17; Fig 9; 82pp; English.
XX
XX The invention describes an isolated polynucleotide encoding an
CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably
CC human; and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This is the amino acid sequence of the autoinducer inactivation protein.
CC AiiG, the autoinducer inactivation activity of which is studied in the
CC invention.
XX
SQ Sequence 250 AA;
Query Match 94.6%; Score 1244; DB 23; Length 250;
Best Local Similarity 92.8%; Pred. No. 9.7e-127;
Matches 232; Conservative 13; Mismatches 5; Indels 0; Gaps 0;
QY 1 MTVKKLYFVPAGRCMLDHSVNSTLTGGLDLFPWCYLLTEEGPILVDTGMPESAVNN 60
DB 1 MTVKKLYFVPAGRCMLDHSVNSALTGKLNLPWCYLLTEEGPILVDTGMPESAVNN 60
QY 61 EGLFNGTFVEGVLPKMTTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
DB 61 EGLFNGTFVEGVLPKMTTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
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DB 121 IIVQRAEYEAHQHSEEVYLKCEILPNLNYKIEGDEVVPGVOLLHTPGHQSLLIET 180
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QY 241 RGCKVFPEYI 250
DB 241 KGCKVFPEYI 250
RESULT 4
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ID AAU78807 standard; Protein; 250 AA.
XX
XX AAU78807;
XX
XX 18-JUN-2002 (first entry)
XX
XX Autoinducer inactivation protein AiiF.
XX
XX Autoinducer inactivation; AiiF; N-acyl-homoserine lactone;

KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; *Erwinia carotovora*.
XX
OS *Bacillus thuringiensis* B17.
XX
PN WO200216623-A1.
XX
XX 28-FEB-2002.
PD
PF 23-AUG-2000; 2000WO-SG00123.
XX
PR 23-AUG-2000; 2000WO-SG00123.
XX
PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX
PI Zhang L, Dong Y, Xu J;
XX
XX WPI; 2002-304123/34.
DR N-PSDB; ABK47471.
XX
XX Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to
PT a disease in sustainable plant or animal and for reducing bacterial
PT damage -
XX
XX Claim 17; Fig 9; 82pp; English.
XX
XX The invention describes an isolated polynucleotide encoding an
CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably
CC human; and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This is the amino acid sequence of the autoinducer inactivation protein.
CC AiiF, the autoinducer inactivation activity of which is studied in the
CC invention.
XX
SQ Sequence 250 AA;
Query Match 93.4%; Score 1228; DB 23; Length 250;
Best Local Similarity 92.8%; Pred. No. 4.8e-125;
Matches 232; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
QY 1 MTVKKLYFVPAGRCMLDHSVNSTLTGGLDLFPWCYLLTEEGPILVDTGMPESAVNN 60
DB 1 MTVKKLYFVPAGRCMLDHSVNSTLTGKLNLPWCYLLTEEGPILVDTGMPESAVNN 60
QY 61 EGLFNGTFVEGVLPKMTTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
DB 61 EGLFNGTFVEGVLPKMTTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
QY 121 IIVQRAEYEAHQHSEEVYLKCEILPNLNYKIEGDEVVPGVOLLHTPGHQSLLIET 180
DB 121 IIVQRAEYEAHQHSEEVYLKCEILPNLNYKIEGDEVVPGVOLLHTPGHQSLLIET 180
QY 181 EKSGPVLTTIDASYTKENFENEFVDFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQE 240
DB 181 EKSGPVLTTIDASYTKENFENEFVDFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQE 240
QY 241 RGCKVFPEYI 250
DB 241 KGCKVFPEYI 250
RESULT 5
AAU78804

ID	AAU78804 standard; Protein; 250 AA.	
XX		
AC	AAU78804;	
XX		
DT	18-JUN-2002 (first entry)	
XX		
DE	Autoinducer inactivation protein AiiC.	
XX		
KW	Autoinducer inactivation; AiiC; N-acyl-homoserine lactone;	
KW	disease resistance; bacterial damage reduction; biofilm;	
KW	potato soft rot disease; Erwinia carotovora.	
XX		
OS	Bacillus thuringiensis Cot1.	
XX		
PN	WO200216623-A1.	
XX		
PD	28-FEB-2002.	
XX		
PF	23-AUG-2000; 2000WO-SG00123.	
XX		
PR	23-AUG-2000; 2000WO-SG00123.	
XX		
PA	(MOLE-) INST MOLECULAR AGROBIOLOGY.	
XX		
PI	Zhang L, Dong Y, Xu J;	
XX		
DR	WPI; 2002-304123/34.	
DR	N-PSDB; ABK47468.	
XX		
PT	Polynucleotide encoding autoinducer inactivation protein, bacterium	
PT	having polynucleotide, and protein useful for increasing resistance to	
PT	a disease in sustainable plant or animal and for reducing bacterial	
PT	damage -	
XX		
PS	Claim 17; Fig 8; 82pp; English.	
XX		
CC	The invention describes an isolated polynucleotide encoding an	
CC	autoinducer (N-acyl-homoserine lactone) inactivation protein. The	
CC	polynucleotide is useful for increasing disease resistance in a plant or	
CC	animal by introducing a polynucleotide into a cell of such a plant or	
CC	animal, in a manner that allows the cell to express the gene. The protein	
CC	is useful for reducing bacterial damage to a plant or animal preferably	
CC	human; and for reducing the formation of bacterial biofilms, by exposing	
CC	biofilm-forming bacteria to the autoinducer inactivation protein. A	
CC	bacterial cell transformed with the polynucleotide, especially a plant or	
CC	animal bacterium preferably Bacillus thuringiensis which is from B1, B2,	
CC	B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a	
CC	disease in a susceptible plant or animal, where virulence is regulated by	
CC	autoinducers e.g. potato soft rot disease caused by Erwinia carotovora.	
CC	This is the amino acid sequence of the autoinducer inactivation protein	
CC	AiiC, the autoinducer inactivation activity of which is studied in the	
XX		
Sequence	250 AA;	
Query Match	92.7%; Score 1219; DB 23; Length 250;	
Best Local Similarity	91.2%; Pred. No. 4.6e-124;	
Matches 228; Conservative	12; Mismatches 10; Indels 0; Gaps 0;	
QY	1 MTVKKLYFVPAACRMLDHSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60	
DB	1 MTVKKLYFVPAACRMLDHSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60	
QY	61 EGLFNGTFFVGGVLPKMTTEEDRIVNILKRVGYEPEDLLYIISHLHFDHAGNGAFINTP 120	
DB	61 ENLFSTFAEGQLLPKMTTEEDRIIALKRAGYEPDLLYIISHLHFDHAGNGAFINTP 120	
QY	121 IIVQAEYEAQAQSHSEYKCEILPNLYKIIEGDYEVVPGVOLLHTPGHTPGHQSLLIET 180	
DB	121 IIVQAEYEAQAQRYEYLKCEILPNLYKIIEGDYEVVPGVOLLHTPGHSPGHQSLLIET 180	
QY	181 EKSGVLLLTIDASYTKENFENVPFAGFDPSELALSSIKRLKEYVMKEKPLVFFGHDIEQE 240	

Db	181 EKSGVLLLTIDASYTKENFENVPFAGFDPSELALSSIKRLKEYVMKEKPLVFFGHDIEQE 240	
QY	241 RGCKVPEYI 250	
DB	241 KGCKVPEYI 250	
RESULT 6		
AAU78806		
ID	AAU78806 standard; Protein; 250 AA.	
XX		
AC	AAU78806;	
XX		
DT	18-JUN-2002 (first entry)	
XX		
DE	Autoinducer inactivation protein AiiE.	
XX		
KW	Autoinducer inactivation; AiiE; N-acyl-homoserine lactone;	
KW	disease resistance; bacterial damage reduction; biofilm;	
KW	potato soft rot disease; Erwinia carotovora.	
XX		
OS	Bacillus thuringiensis B2.	
XX		
PN	WO200216623-A1.	
XX		
PD	28-FEB-2002.	
XX		
PF	23-AUG-2000; 2000WO-SG00123.	
XX		
PR	23-AUG-2000; 2000WO-SG00123.	
XX		
PA	(MOLE-) INST MOLECULAR AGROBIOLOGY.	
XX		
PI	Zhang L, Dong Y, Xu J;	
XX		
DR	WPI; 2002-304123/34.	
DR	N-PSDB; ABK47470.	
XX		
PT	Polynucleotide encoding autoinducer inactivation protein, bacterium	
PT	having polynucleotide, and protein useful for increasing resistance to	
PT	a disease in sustainable plant or animal and for reducing bacterial	
PT	damage -	
XX		
PS	Claim 17; Fig 9; 82pp; English.	
XX		
CC	The invention describes an isolated polynucleotide encoding an	
CC	autoinducer (N-acyl-homoserine lactone) inactivation protein. The	
CC	polynucleotide is useful for increasing disease resistance in a plant or	
CC	animal by introducing a polynucleotide into a cell of such a plant or	
CC	animal, in a manner that allows the cell to express the gene. The protein	
CC	is useful for reducing bacterial damage to a plant or animal preferably	
CC	human; and for reducing the formation of bacterial biofilms, by exposing	
CC	biofilm-forming bacteria to the autoinducer inactivation protein. A	
CC	bacterial cell transformed with the polynucleotide, especially a plant or	
CC	animal bacterium preferably Bacillus thuringiensis which is from B1, B2,	
CC	B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a	
CC	disease in a susceptible plant or animal, where virulence is regulated by	
CC	autoinducers e.g. potato soft rot disease caused by Erwinia carotovora.	
CC	This is the amino acid sequence of the autoinducer inactivation protein	
CC	AiiE, the autoinducer inactivation activity of which is studied in the	
XX		
Sequence	250 AA;	
Query Match	92.2%; Score 1213; DB 23; Length 250;	
Best Local Similarity	90.4%; Pred. No. 2.1e-123;	
Matches 226; Conservative	14; Mismatches 10; Indels 0; Gaps 0;	
QY	1 MTVKKLYFVPAACRMLDHSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60	
DB	1 MTVKKLYFVPAACRMLDHSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60	
QY	61 EGLFNGTFFVGGVLPKMTTEEDRIVNILKRVGYEPEDLLYIISHLHFDHAGNGAFINTP 120	

Db 61 EGLFNGTVEGQILPMTTEEDRIIVNLKRVGYEPDPLLIISSHLHFDHAGNGAFTNTP 120
 QY 121 IIVQRAEYEAQHSEYLYKECILPNLYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIET 180
 Db 121 IIVQTEYEAALHREYMKECILPHLYKIIEGDYEVVPGVQLLHTPGHSPGHQSILFIET 180
 QY 181 EKSGPVLLTIDASYTKENFENEPAGPDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
 Db 181 EOGSGVLLTIDASYTKENFEDEVPPAGDPPELALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
 QY 241 RGCKVFPEYI 250
 Db 241 KSCRVFPEYI 250

RESULT 7
 AAU78809
 ID AAU78809 standard; Protein; 250 AA.

AC AAU78809;

DT 18-JUN-2002 (first entry)

DE Autoinducer inactivation protein AiiH.

XX Autoinducer inactivation; AiiH; N-acyl-homoserine lactone;
 KW disease resistance; bacterial damage reduction; biofilm;
 KW potato soft rot disease; Erwinia carotovora.

OS Bacillus thuringiensis B20.

PN WO200216623-A1.

PD 28-FEB-2002.

XX 23-AUG-2000; 2000WO-SG00123.

XX 23-AUG-2000; 2000WO-SG00123.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX Zhang L, Dong Y, Xu J;

XX WPI; 2002-304123/34.

XX N-PSDB; ABK47473.

XX Polynucleotide encoding autoinducer inactivation protein, bacterium
 PT having polynucleotide, and protein useful for increasing resistance to
 PT a disease in sustainable plant or animal and for reducing bacterial
 PT damage -

XX Claim 17; Fig 9; 82pp; English.

XX The invention describes an isolated polynucleotide encoding an
 CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
 CC polynucleotide is useful for increasing disease resistance in a plant or
 CC animal by introducing a polynucleotide into a cell of such a plant or
 CC animal, in a manner that allows the cell to express the gene. The protein
 CC is useful for reducing bacterial damage to a plant or animal preferably
 CC human; and for reducing the formation of bacterial biofilms, by exposing
 CC biofilm-forming bacteria to the autoinducer inactivation protein. A
 CC bacterial cell transformed with the polynucleotide, especially a plant or
 CC animal bacterium preferably *Bacillus thuringiensis*, which is from B1, B2,
 CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
 CC disease in a susceptible plant or animal, where virulence is regulated by
 CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
 CC This is the amino acid sequence of the autoinducer inactivation protein
 CC AiiH, the autoinducer inactivation activity of which is studied in the
 CC invention.

XX Sequence 250 AA;

Query Match 92.2%; Score 1212; DB 23; Length 250;
 Best Local Similarity 90.8%; Pred. No. 2.7e-123;
 Matches 227; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTVKKLYFVAGRCMLDSSVNSTLTGCELLDLPVWCYLLTEEGPILVDTGMPESAVNN 60
 Db 1 MTVKKLYFVAGRCMLDSSVNSTLTGCELLDLPVWCYLLTEEGPILVDTGMPESAVNN 60
 QY 61 EGLFNGTVEGQILPMTTEEDRIIVNLKRVGYEPDPLLIISSHLHFDHAGNGAFTNTP 120
 Db 61 EGLFNGTVEGQILPMTTEEDRIIVNLKRVGYEPDPLLIISSHLHFDHAGNGAFTNTP 120
 QY 121 IIVQRAEYEAQHSEYLYKECILPNLYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIET 180
 Db 121 IIVQRAEYEAALHREYMKECILPHLYKIIEGDYEVVPGVQLLHTPGHSPGHQSILFIET 180
 QY 181 EKSGPVLLTIDASYTKENFENEPAGPDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
 Db 181 EOGSGVLLTIDASYTKENFEDEVPPAGDPPELALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
 QY 241 RGCKVFPEYI 250
 Db 241 KSCRVFPEYI 250

RESULT 8

AAU78811

ID AAU78811 standard; Protein; 250 AA.

AC AAU78811;

DT 18-JUN-2002 (first entry)

DE Autoinducer inactivation protein AiiJ.

KW Autoinducer inactivation; AiiJ; N-acyl-homoserine lactone;
 KW disease resistance; bacterial damage reduction; biofilm;
 KW potato soft rot disease; Erwinia carotovora.

OS Bacillus thuringiensis B22.

PN WO200216623-A1.

PD 28-FEB-2002.

XX 23-AUG-2000; 2000WO-SG00123.

XX 23-AUG-2000; 2000WO-SG00123.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX Zhang L, Dong Y, Xu J;

XX WPI; 2002-304123/34.

XX N-PSDB; ABK47475.

XX Polynucleotide encoding autoinducer inactivation protein, bacterium
 PT having polynucleotide, and protein useful for increasing resistance to
 PT a disease in sustainable plant or animal and for reducing bacterial
 PT damage -

XX Claim 17; Fig 9; 82pp; English.

XX The invention describes an isolated polynucleotide encoding an
 CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
 CC polynucleotide is useful for increasing disease resistance in a plant or
 CC animal by introducing a polynucleotide into a cell of such a plant or
 CC animal, in a manner that allows the cell to express the gene. The protein
 CC is useful for reducing bacterial damage to a plant or animal preferably
 CC human; and for reducing the formation of bacterial biofilms, by exposing
 CC biofilm-forming bacteria to the autoinducer inactivation protein. A
 CC bacterial cell transformed with the polynucleotide, especially a plant or
 CC animal bacterium preferably *Bacillus thuringiensis*, which is from B1, B2,

XX PT Polynucleotide encoding autoinducer inactivation protein, bacterium
 PT having polynucleotide, and protein useful for increasing resistance to
 PT a disease in sustainable plant or animal and for reducing bacterial
 PT damage -
 XX
 XX Claim 17; Fig 9; 82pp; English.
 XX
 XX The invention describes an isolated polynucleotide encoding an
 CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
 CC polynucleotide is useful for increasing disease resistance in a plant or
 CC animal by introducing a polynucleotide into a cell of such a plant or
 CC animal, in a manner that allows the cell to express the gene. The protein
 CC is useful for reducing bacterial damage to a plant or animal preferably
 CC human; and for reducing the formation of bacterial biofilms, by exposing
 CC biofilm-forming bacteria to the autoinducer inactivation protein. A
 CC bacterial cell transformed with the polynucleotide, especially a plant or
 CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
 CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
 CC disease in a susceptible plant or animal, where virulence is regulated by
 CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
 CC This is the amino acid sequence of the autoinducer inactivation protein
 CC AiiD, the autoinducer inactivation activity of which is studied in the
 CC invention.
 XX
 XX Sequence 250 AA;
 XX
 XX Query Match 91.4%; Score 1202; DB 23; Length 250;
 XX Best Local Similarity 89.6%; Pred. No. 3.3e-122;
 XX Matches 224; Conservative 14; Mismatches 12; Indels 0; Gaps 0;
 XX
 XX 1 MTVKKLYFVPAGRCLMDHSSVNSTLTGCELDLPVWCYLLETEGPIILVDTGMPESAVNN 60
 XX Db 1 MTVKKLYFIPAGRCMLDSSVNSAUTPGKLNLPVWCYLLETEGPIILVDTGMPESAVNN 60
 XX
 XX 61 EGLFNGTFVEGQVLPKMTTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 XX Db 61 EGLFNGTFVEGQVLPKMTTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 XX
 XX 121 IIVQRAEYEAQHSEYVKECILPNLNYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIET 180
 XX Db 121 IIVQTEYEAAALHREYMKECILPHLNKYKIIEGDYEVVPGVQLLHTPGHSPGHSLSFIET 180
 XX
 XX 181 EKSGPVLTLTIDASYTKENFENFVPPAGFDSFELALSSIKRLKEVVMKEKPIVFFGHDIEQE 240
 XX Db 181 EQSGVLMLIDASYTKENFENFVPPAGFDPPELAUSSIKRLKEVVMKEKPIIFFFGHDTEQE 240
 XX
 XX 241 RGCKVFPEYI 250
 XX Db 241 KSCRVFPEYI 250
 XX
 XX RESULT 11
 XX AAU78812
 XX ID AAU78812 standard; Protein; 250 AA.
 XX
 XX AC AAU78812;
 XX
 XX 18-JUN-2002 (first entry)
 XX
 XX Autoinducer inactivation protein AiiK.
 XX
 XX Autoinducer inactivation; AiiK; N-acyl-homoserine lactone;
 XX disease resistance; bacterial damage reduction; biofilm;
 XX potato soft rot disease; *Erwinia carotovora*.
 XX
 XX *Bacillus thuringiensis* B25.
 XX
 XX WO200216623-A1.
 XX
 XX 28-FEB-2002.
 XX
 XX 23-AUG-2000; 2000WO-SG00123.

XX PR 23-AUG-2000; 2000WO-SG00123.
 XX XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
 XX PA Zhang L, Dong Y, Xu J;
 XX PI WPI; 2002-304123/34.
 XX DR N-PSDB; ABK47476.
 XX
 XX Polynucleotide encoding autoinducer inactivation protein, bacterium
 PT having polynucleotide, and protein useful for increasing resistance to
 PT a disease in sustainable plant or animal and for reducing bacterial
 PT damage -
 XX
 XX Claim 17; Fig 9; 82pp; English.
 XX
 XX The invention describes an isolated polynucleotide encoding an
 CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
 CC polynucleotide is useful for increasing disease resistance in a plant or
 CC animal by introducing a polynucleotide into a cell of such a plant or
 CC animal, in a manner that allows the cell to express the gene. The protein
 CC is useful for reducing bacterial damage to a plant or animal preferably
 CC human; and for reducing the formation of bacterial biofilms, by exposing
 CC biofilm-forming bacteria to the autoinducer inactivation protein. A
 CC bacterial cell transformed with the polynucleotide, especially a plant or
 CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
 CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
 CC disease in a susceptible plant or animal, where virulence is regulated by
 CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
 CC This is the amino acid sequence of the autoinducer inactivation protein
 CC AiiK, the autoinducer inactivation activity of which is studied in the
 CC invention.
 XX
 XX Sequence 250 AA;
 XX
 XX Query Match 91.3%; Score 1200; DB 23; Length 250;
 XX Best Local Similarity 90.0%; Pred. No. 5.4e-122;
 XX Matches 225; Conservative 12; Mismatches 13; Indels 0; Gaps 0;
 XX
 XX 1 MTVKKLYFVPAGRCLMDHSSVNSTLTGCELDLPVWCYLLETEGPIILVDTGMPESAVNN 60
 XX Db 1 MTVKKLYFIPAGRCMLDSSVNGTAPGNLNLVWCYLLETEGAILVDTGMPESAVNN 60
 XX
 XX 61 EGLFNGTFVEGQVLPKMTTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 XX Db 61 EGLFNGTFVEGQVLPKMTTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 XX
 XX 121 IIVQRAEYEAQHSEYVKECILPNLNYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIET 180
 XX Db 121 IIVQTEYEAAALHREYMKECILPHLNKYKIIEGDYEVVPGVQLLHTPGHSPGHSLSFIET 180
 XX
 XX 181 EKSGPVLTLTIDASYTKENFENFVPPAGFDSFELALSSIKRLKEVVMKEKPIVFFGHDIEQE 240
 XX Db 181 EQSGSVLLTIDASYTKENFENFVPPAGFDPPELAUSSIKRLKEVVMKEKPIVFFGHDIEQE 240
 XX
 XX 241 RGCKVFPEYI 250
 XX Db 241 KGCVRVPEYI 250
 XX
 XX RESULT 12
 XX AAU78815
 XX ID AAU78815 standard; Protein; 263 AA.
 XX
 XX AC AAU78815;
 XX
 XX 18-JUN-2002 (first entry)
 XX
 XX Autoinducer inactivation protein AiiB.
 XX
 XX Autoinducer inactivation; AiiB; N-acyl-homoserine lactone;
 XX disease resistance; bacterial damage reduction; biofilm;

[illegible]

